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_____ A.A. Sequence
_____ Structure
_____ Bibliographic

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_____ SDC
_____ DARC/Questel
✓ _____ Other CGN

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Ka1115
09/12/8412
Seq. ID 1 w/ Interf
Page 1

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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:13:53 ; Search time 3186 Seconds

(without alignments)
7796.854 Million cell updates/sec

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Perfect score: 988
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Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 08
Maximum Match 108

Listing first 45 summaries

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3	516.2	52.2	672	1	PCT-US02-27884-3352	Sequence 3352, Ap	
4	490.2	49.6	623	1	PCT-US02-27884-5530	Sequence 5530, Ap	
5	401.2	40.0	734	28	US-09-705-926-4708	Sequence 4708, Ap	
6	385.8	39.0	632	1	PCT-US02-27884-3350	Sequence 3350, Ap	
7	371.6	37.6	618	28	US-09-705-926-3115	Sequence 3115, Ap	
8	343.4	34.8	994	41	US-10-155-881-36087	Sequence 36087, A	
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12	339.6	34.4	973	75	US-09-312-544-1609	Sequence 1609, Ap	
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15	338.6	34.3	1006	29	US-09-733-089-12353	Sequence 12353, A	
16	338.6	34.3	1006	31	US-09-816-660-12353	Sequence 12353, A	
17	336.4	34.0	983	1	PCT-US00-06112-15	Sequence 15, Appl	
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25 334.2 33.8 1042 25 US-09-654-617-124315 Sequence 124315, A
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29 333 33.7 578 1 PCT-US02-27884-1066 Sequence 1066, Ap
30 332 33.6 570 22 US-09-565-309A-66976 Sequence 66976, A
31 332 33.6 969 19 US-09-513-996A-2994 Sequence 2994, Ap
32 332 33.6 969 22 US-09-565-309A-52278 Sequence 52278, A
33 332 33.6 969 22 US-09-565-309A-61940 Sequence 61940, A
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35 331 33.5 886 19 US-09-513-996A-9337 Sequence 9337, Ap
36 330.8 33.5 711 33 US-09-874-708A-64616 Sequence 64616, A
37 330.8 33.5 711 65 US-09-611-750-63529 Sequence 63529, A
38 330.4 33.4 747 33 US-09-874-708A-69304 Sequence 69304, A
39 330.4 33.4 747 65 US-60-211-750-68217 Sequence 68217, A
40 329 33.3 1191 41 US-10-155-881-15913 Sequence 15913, A
41 324.4 32.8 701 23 US-09-605-702-10495 Sequence 10495, A
42 324.4 32.8 701 23 US-09-611-520-9806 Sequence 9806, Ap
43 324.4 32.8 701 58 US-10-075-564-9806 Sequence 9806, Ap
44 324.4 32.8 701 58 US-60-146-224-6858 Sequence 6858, Ap
45 324 32.8 521 1 PCT-US02-27884-3353 Sequence 3353, Ap

ALIGNMENTS

RESULT 1
US-09-928-412-1

Sequence 1, Application US/09928412
GENERAL INFORMATION:
APPLICANT: KAWAOKA, Akiyoshi
APPLICANT: EBINUMA, Hiroyasu
TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
TITLE OF INVENTION: BIOSYNTHESIS PATHWAY
FILE REFERENCE: 4859-0027-0
CURRENT APPLICATION NUMBER: US/09/928,412
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/282,146
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-125171
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 988
TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: CDS
LOCATION: (100)..(702)
NAME/KEY: misc_feature
LOCATION: (127)..(282)
OTHER INFORMATION: LIM domain
NAME/KEY: misc_feature
LOCATION: (427)..(582)
OTHER INFORMATION: LIM domain
US-09-928-412-1

Query Match 100.0%; Score 988; DB 34; Length 988;
Best Local Similarity 100.0%; Pred. No. 1.2e-234;
Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGCGCCGTCACAAACCAAGTGTACACAAAGGGAAGGCCACCAAG 60
DB 1 GATTCGGCGCCGTCACAAACCAAGTGTACACAAAGGGAAGGCCACCAAG 60
QY 61 ACCATTTTCTTTCTGTAAACCTGCTATATAGCCATGGCTTTGGAGAACACA 120
DB 61 ACCATTTTCTTTCTGTAAACCTGCTATATAGCCATGGCTTTGGAGAACACA 120

QY 121 CAGAAATGCATGCATGTGACAAAGCTGTATCTGTGTGACAAATTAAGTCAGATTAAC 180
DB 121 CAGAAATGCATGCATGTGACAAAGCTGTATCTGTGTGACAAATTAAGTCAGATTAAC 180
QY 181 AGAATCTATACAAAGCTGTGTGACATGCATGCATGCATGCATGCATGCATGCATGC 240
DB 181 AGAATCTATACAAAGCTGTGTGACATGCATGCATGCATGCATGCATGCATGCATGC 240
QY 241 AACTACATTCCTTTGAGCGAGCTTCTATCTGTAGACACACTTTGATTCAGCTTTGAAA 300
DB 241 AACTACATTCCTTTGAGCGAGCTTCTATCTGTAGACACACTTTGATTCAGCTTTGAAA 300
QY 301 CAATCGGCACTTTGGATTAAGCTTTGAGAGTACACCAAAAATGTGAAGCCACAGAAA 360
DB 301 CAATCGGCACTTTGGATTAAGCTTTGAGAGTACACCAAAAATGTGAAGCCACAGAAA 360
QY 361 CCCATTGACATGTGAAGAACCCAGCTGACCAATGACCAATGACCAATGACCAATGACCA 420
DB 361 CCCATTGACATGTGAAGAACCCAGCTGACCAATGACCAATGACCAATGACCAATGACCA 420
QY 421 GAGAAATGTTTGGCTGCAAGAAACTGTCTACCCACAGAAAGTATCAGCCATGGC 480
DB 421 GAGAAATGTTTGGCTGCAAGAAACTGTCTACCCACAGAAAGTATCAGCCATGGC 480
QY 481 AGCCCATACATTAAGAGCTGCTCAATTCAGACGAGGAGCTGTATTAAGCCCTTCC 540
DB 481 AGCCCATACATTAAGAGCTGCTCAATTCAGACGAGGAGCTGTATTAAGCCCTTCC 540
QY 541 AACTATACCGCAGATGAGGGGCGCTTATTTGTAAATCAATCAATCAATCAATCAATCA 600
DB 541 AACTATACCGCAGATGAGGGGCGCTTATTTGTAAATCAATCAATCAATCAATCAATCA 600
QY 601 GAGAAAGGCAACTTAAGCAAGCTTTGAGGGGTGACCCATGAATTAATTCACAGACAAACA 660
DB 601 GAGAAAGGCAACTTAAGCAAGCTTTGAGGGGTGACCCATGAATTAATTCACAGACAAACA 660
QY 661 GGAATTACTGACAGATCATACACAGCCGACCAAGTATGATCTTATTCACGCGCA 720
DB 661 GGAATTACTGACAGATCATACACAGCCGACCAAGTATGATCTTATTCACGCGCA 720
QY 721 TCATGTATTCGATTCGCTGTGTGTTGTTGAAGATGCAAGGCGTTCAGAGCTTCATGA 780
DB 721 TCATGTATTCGATTCGCTGTGTGTTGTTGAAGATGCAAGGCGTTCAGAGCTTCATGA 780
QY 781 ATGCATTTGCCCTGCCACGATGTTTACTTAATTAATTAATTAATTAATTAATTAAT 840
DB 781 ATGCATTTGCCCTGCCACGATGTTTACTTAATTAATTAATTAATTAATTAATTAAT 840
QY 841 TGAACATATATATGCTAGCTTTTGTGTGATTTTGAACCTTTGCTTGTGCTTC 900
DB 841 TGAACATATATATGCTAGCTTTTGTGTGATTTTGAACCTTTGCTTGTGCTTC 900
QY 901 ACTGTATTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 960
DB 901 ACTGTATTTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 960
QY 961 ATGCAAACTTTGAGCGCGCGCAATTC 988
DB 961 ATGCAAACTTTGAGCGCGCGCAATTC 988

RESULT 2
PCT-US02-27884-5525

Sequence 5525, Application PC/TUS0227884
GENERAL INFORMATION:
APPLICANT: The Dow Chemical Company
APPLICANT: Dow Agro Sciences, LLC
TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Character
FILE REFERENCE: DOW-07611
CURRENT APPLICATION NUMBER: PCT/US02/27884
NUMBER OF SEQ ID NOS: 7560
SOFTWARE: PatentIn version 3.1

Query Match 49.6%; Score 490.2; DB 1; Length 623;
 Best Local Similarity 89.6%; Pred. No. 5e-111;
 Matches 560; Conservative 0; Mismatches 38; Indels 27; Gaps 2;

QY 87 CTCCTATATAGCATGGCTTTTGCAGAACACAGAAATGATGGCATGTGACAAAC 146
 DB 1 CTCATATATAGCATGGCTTTTGCAGAACACACAGAAATGATGGCATGTGACAAAC 60
 QY 147 TGTCTATCTGTGACAAATTAAGTACAGATACAGAAATCTATACAAAGCTTTTCAG 206
 DB 61 TGTCTATCTGTGACAAATTAAGTACAGATACAGAAATCTATACAAAGCTTTTCAG 120
 QY 207 ATGCCATCAGTCAGAGGCACTGTCAAGCTTGGCACTACATCTTTTGGAGAGTTCT 266
 DB 121 ATGCCATCAGTCAGAGGCACTGTCAAGCTTGGCACTACATCTTTTGGAGAGTTCT 180
 QY 267 ATACTGTAGACACACTTTGTATCAGCTCTTCAACCAAACTGGAGTTGGATTAAGCTT 326
 DB 181 ATACTGTAGACACACTTTGTATCAGCTCTTCAACCAAACTGGAGTTGGATTAAGCTT 240
 QY 327 TGAAGGTACACAAAATATGTGAAGCCAGAAACCCATGGACAGTGAAGAACCAAGT 386
 DB 241 TGA-----AGAAACCATTTGACACTGAGAAACCAAGT 274
 QY 387 AGCCAAAGTGCAGACATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAAC 446
 DB 275 AGCTAAAGTGCAGACATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAAC 334
 QY 447 TGTCTACCAACAGAAAGATATGAGCAATGAGCAGCATATCATTAAAGCTCTTCCA 506
 DB 335 TGTCTACCAACAGAAAGATATGAGCAATGAGCAGCATATCATTAAAGCTCTTCCA 394
 QY 507 ATGAGCCAGAGAGCTGTGTATATAGCCCTTCCACTATACCCAGATGAGGGCCCTT 566
 DB 395 ATGAGCCAGAGAGCTGTGTATATAGCCCTTCCACTATACCCAGATGAGGGCCCTT 454
 QY 567 ATATGTAAACATCACCATTATTCACCTTATCAGAGAGAGGCACTTAAGCAAGCTTGA 626
 DB 455 CTACTGTAAACATCACCATTATTCACCTTATCAGAGAGAGGCACTTAAGCAAGCTTGA 514
 QY 627 GGGTGACCATGAATTAATTCACAGACACAGAGATTACTCAGAGATCATACAGC 686
 DB 515 GGGTGACCATGAATTAATTCACAGACACAGAGATTACTCAGAGATCATACAGC 573
 QY 687 CGACCAAGTTGATGATCCTTATCT 711
 DB 574 CGACCAAGTTGATGATCCTTATCT 598

RESULT 5
 US-09-705-926-4708/c
 ; Sequence 4708, Application US/09705926
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Liu, Jingtong
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: ANNOTATED PLANT GENES
 ; FILE REFERENCE: 38-21(15481)A
 ; CURRENT APPLICATION NUMBER: US/09/705,926
 ; CURRENT FILING DATE: 2000-11-06
 ; NUMBER OF SEQ ID NOS: 21634
 ; SEQ ID NO 4708
 ; LENGTH: 734
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 US-09-705-926-4708

Query Match 40.6%; Score 401.2; DB 28; Length 734;
 Best Local Similarity 81.1%; Pred. No. 6.9e-89;
 Matches 482; Conservative 0; Mismatches 103; Indels 9; Gaps 1;

QY 71 TTTTCTGTAAACTGTGCTGTATATAGCATGGCTTTTGCAGAACACACAGAAATGCA 130
 DB 1 TTTTCTGTAAACTGTGCTGTATATAGCATGGCTTTTGCAGAACACACAGAAATGCA 130

DB 733 TTTTCTGTAAACTGTGCTGTATATAGCATGGCTTTTGCAGAACACACAGAAATGCA 674
 QY 131 TGGCATGTGACAAAGTGTCTATCTGTGACAAATTAAGTACAGATACAGAAATCTATC 190
 DB 673 TGGCATGTGACAAAGTGTCTATCTGTGACAAATTAAGTACAGATACAGAAATCTATC 614
 QY 191 ACAAGCTTTGTTAGATGCCATCAGTCAAGGCGACTGTCAAGCTTTGGCAACTACATTT 250
 DB 613 ATAAAGCTTTGTTAGATGCCATCAGTCAAGGCGACTGTCAAGCTTTGGCAACTACATTT 554
 QY 251 CCTTGGAGGAGTCTTATCTATCTAGTACACCTTGTATGAGCTCTTCAACCAACTGCA 310
 DB 553 CATTTGAGGAGTCTTATCTATCTAGTACACCTTGTATGAGCTCTTCAACCAACTGCA 494
 QY 311 GTTTGATTAAGCTTTGAAAGTACACCAAAATTAAGTGAAGCCAGCAAAACCCATTTGCA 370
 DB 493 GTTTGATTAAGCTTTGAAAGTACACCAAAATTAAGTGAAGCCAGCAAAACCCATTTGCA 443
 QY 371 GTGAAACACAGAGTGTGCAAGAGTGAACATGTTTGGTGAAGAGAGAAATGTTT 430
 DB 442 ATGAAACACAGAGTGTGCAAGAGTGAACATGTTTGGTGAAGAGAGAAATGTTT 383
 QY 431 TTGGCTGCAAGAAACCTGTCTATCTATCTCAACAGAAAGTATCAGCAATGGCAGCATATCC 490
 DB 382 TTGGCTGCAAGAAACCTGTCTATCTATCTCAACAGAAAGTATCAGCAATGGCAGCATATCC 323
 QY 491 ATAAAGCTCTCTTCAATGAGCAGCAGGAGGCTGTGAATTAAGCCCTTCCAACTATACCG 550
 DB 322 ACAAAAGCTCTCTTCAATGAGCAGCAGGAGGCTGTGAATTAAGCCCTTCCAACTATATTCG 263
 QY 551 CACATGAGGAGGCTGTATATTTGAACATCACCATTATTCACCTTATTCAGAGAGAGGCA 610
 DB 262 CTCAGAGAGGAGGCTGTATATTTGAACATCACCATTATTCACCTTATTCAGAGAGAGGCA 203
 QY 611 ACTTAACCAAGCTTGAAGGTGACCATTAATGAATTCACAGACACACAGAGAG 664
 DB 202 ACTTAACCAAGCTTGAAGGTGACCATTAATGAATTCACAGACACACAGAGAG 149

RESULT 6
 PCT-US02-27884-3350
 ; Sequence 3350, Application PC/TUS0227884
 ; GENERAL INFORMATION:
 ; APPLICANT: The Dow Chemical Company
 ; APPLICANT: Dow Agro Sciences, LLC
 ; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Character
 ; FILE REFERENCE: DOW-07611
 ; CURRENT APPLICATION NUMBER: PCT/US02/27884
 ; CURRENT FILING DATE: 2002-08-30
 ; NUMBER OF SEQ ID NOS: 7560
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3350
 ; LENGTH: 632
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 PCT-US02-27884-3350

Query Match 39.0%; Score 385.8; DB 1; Length 632;
 Best Local Similarity 83.4%; Pred. No. 4.4e-85;
 Matches 466; Conservative 0; Mismatches 82; Indels 11; Gaps 2;

QY 98 CCATGGCTTTTGCAGAACACAGAAATGATGGATGTGACAGTGTATCTG 157
 DB 85 CCATGGCTTTTGCAGAACACAGAAATGATGGATGTGACAGTGTATCTG 142
 QY 158 TTGACAAATTAAGTGTGACAGATACAGATATATCAAGAGCTTTTGCAGATGCACT 217
 DB 143 TTGACAAATTAAGTGTGACAGATACAGATATATCAAGAGCTTTTGCAGATGCACT 202
 QY 218 GCAAGGCACTGTCAAGCTTTGCAACTACATTTCTTTGAGGAGGTTCTATCTGAGAC 277
 DB 1 GCAAGGCACTGTCAAGCTTTGCAACTACATTTCTTTGAGGAGGTTCTATCTGAGAC 277

Db	203	GCAGGGTACTCTCAGGTTTGGCACTACATTAATTATTGGAGGAGTTCTCTATTGTAGAC	262
Oy	278	CACACTTTGATCAGCTCTTCAACCAACTGGCAGTTTGGATTAAGAAGCTTGAAGGTACAC	337
Db	263	CTCACTTTGATCAGCTCTTTTAAAGAAGTGGAACTGTGGACAAAGCTTTGAAGGGGAC	322
Oy	338	CAAAAAATGTAACCCACAGAAACCCATTGCAGTGGAAAAACCAAGGTAGCCAAAGTGA	397
Db	323	CCAAAATTTGTAAACCCAGAGAAA-----GATGGAAAAACCAACATGCTGTAAAGTCT	373
Oy	398	CAAGCATTTTGGTGGAAACAGAGAGAAATTTTGGCTGCAGAAAGAACTGTACACAA	457
Db	374	CAAGCATTTTGGTGGAAACAGAGAGAAATTTTGGCTGCAGAAATACGTCTATGCCAA	433
Oy	458	CAGAAAAGGTATCAGCCCAAGTGGACGCCCATACCTAAGAGCTGCTTCAATGCAAGCCAG	517
Db	434	CAGAAAAGGTATCAGTGAATTTGAACACCATATTCACAAAAGCTGCTCAAAATGTAGCCATG	493
Oy	518	GAGGCTGTATTAAGCCCTTCACAATATACCCGACATGAGGGGGGCGCTTATATTGTTAAAC	577
Db	494	GTGGATGCAACAATTAAGCCCATTCACATATATTGTGGCACAGGGGGGCGCTTTACTGCAAAC	553
Oy	578	ATCACCATATTCACATTAATCAAGAGAGAAAGGCACTTAAGCAAGCTTGAAGGATGCACATG	637
Db	554	ATCACCATATTCACATTAATCAAGAGAGAAAGCAACTTAAGCCACACTGAGAGGGATCATGTG	613
Oy	638	AAATGAATTCACAGCAAC 656	
Db	614	ACAAGAAATACAGTTAGAAC 632	

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RESULT 7
US-09-705-926-3115
; Sequence 3115, Application US/09705926
; GENERAL INFORMATION:
; APPLICANT:          Rovallic, David K.
; APPLICANT:          Liu, Jingdong
; APPLICANT:          Wiegand, Roger C.
; TITLE OF INVENTION: ANNOTATED PLANT GENES
; FILE REFERENCE:      38-21(15481)A
; CURRENT APPLICATION NUMBER: US/09/705,926
; CURRENT FILING DATE:  2000-11-06
; NUMBER OF SEQ ID NOS: 21634
; SEQ ID NO 3115
; LENGTH: 618
; TYPE: DNA
; ORGANISM: Lycopodium obscurum
US-09-705-926-3115

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Query Match	37.68	Score 371.6	DB 28	Length 618
Best Local Similarity	89.28	Pred. NO. 1.5e-81		
Matches 423; Conservative	0	Mismatches 49	Indels 2	Gaps 2

QY	93	TATAGCCATGGCTTTTGTGAGAACCCACAGAAATTCATGGCATGTGTACAAAGACTGCTA	1522
Db	144	TATAGCCATGGCATTTTGTGAGAACCAACAAATGGATGGCTTGTACAAAGACTGCTCA	2030
QY	153	TCTGTGTACCAATTAATCTGCAGATTAACAGAAATCTATCACAAAGCTGTTTCAGATGCCA	2122
Db	204	TCTGGCTGCACAGGTTAACTGCAAGATTAACAGAAATCTATCACAAAGCTGTTTAAATGTCA	2633
QY	213	TCACTGCAAGGGCACCTGTCAAGCTTGGCACTACAAATTCCTTTGAGGGAGTCTATACGTG	2727
Db	264	TCACGCAAGGGCACCCCTCAAGCTTGGCACTACAAATTCCTTTGAAAGAGACTCTGTACTG	3233
QY	273	TAGACACAA -CTTTGATCAGCTCTTCAACAAACTGGCAGTTGGATTAAGAGCTTTAAAG	3312
Db	324	TAGACACAACTTTGTATGAGCTCTTCAACAAACTGGCAGCTTGGATTAAGAGCTTTTGAAG	3833
QY	332	GTACACCAAAAAATGTGAAGCCACAGAAACCCTATGACAGTGAAGAACCA -CAGGTAGCC	3902
Db	384	GTACACCAAAAAATGTGAAGCCACAGAAAGCTCATTTGACAGTGAAGAACCAACCAGGTAGCT	4433

QY	391	AAAGTGACAGCAGTCATGTTGGTGGGAACAAGAGAGAAATGTTTGGCTGCAGAAAGAACTGTC	450
Db	444	AAAGGACACAGCATGTTGGTGGGAACAAGGAGAAATGTTTGGCTGCCAGAACACTGTC	503
QY	451	TACCCACAGAAAAGGTATTCAGCCAAATGGCAGCCATATCCATTAAGAGCTGCTTCCAAATGC	510
Db	504	TATCCACAGAAAGGTATTCAGTTAATGTGACACATACCAACAAAACACTGCTTCAAAATGT	563
QY	511	AGCCACGGAGGCTGTGTATATTAAGCCCTTCCACACTATATCCGACATGAGGGGGCG	564
Db	564	AGCCATGGAGGGGTGTATTAATAGCTTTCACCTCTATGTGACATGGAAGGGGGCG	617

RESULT 8
US-10-155-881-36087
; Sequence 36087, Application US/10155881

```

/ APPLICANT: Ooston, Stanton B.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Lutfiyya, Linda L.
/ APPLICANT: McIninch, James
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
/ TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
/ FILE REFERENCE: 38-21(1530)J
/ CURRENT APPLICATION NUMBER: US/10/155,881
/ CURRENT FILING DATE: 2002-05-22
/ NUMBER OF SEQ ID NOS: 37595
/ SEQ ID NO 36087
/ LENGTH: 994
/ TYPE: DNA
/ ORGANISM: Glycine max
US-10-155-881-36087

```

Query Match	34.8%;	Score 343.4;	DB 41;	Length 994;
Best Local Similarity	77.6%;	Pred. No. 1.7e-74;		
Matches 429; Conservative	0;	Mismatches 121;	Indels 3;	Gaps 1

Qy	100	ATGCGTTTGGAGGACCACACACAAATGCAATGCAATGCAAGACTGCTATCGGTT	159
Db	164	ATGGCATTTTGGACGAAACACACAGAAAGTATATGCGCTGTGACAAACCGTTTATCTGTT	223
Qy	160	GACCAATTTAACTGCGAGATTAACGATATCATCCAAAGCTGTGTTTCAGATGCGATCATGCG	219
Db	224	GATATGTTGACCGCGGATTAACCGAGTTTCCACAAAGGTTGCTTCAGATGCGATCATGCG	283
Qy	220	AAGGCACTGTCAGACTTGGCACTACATATCTTTGAGGAGGTTCTATCTATGACCA	279
Db	284	AAAGGAACCTTCACAGCTGAGAACCTACCAACTTTTGAAGGAGTCTTTTATTTGAAACCA	343
Qy	280	CACCTTGCATCAGCTCTTGAACAACTGCGAGTTTGGATTAACCTTTGAAGGTACCA	339
Db	344	CACCTTGAACCAACTGTTCAAAAGAACAGGAGCCTTGACAAACCTTTGAAGGAACACA	403
Qy	340	AAAAATGTGAAGCCACAGAAACCCATTGACAGTGAAGAAACACAGTAAGCCAAAGTACA	399
Db	404	AAAAATGGCAAGCCGAGAAATAATTTGGA---AGAGAAACCTGACAGCAACCAAGTCTCA	460
Qy	400	ASCATGTTTGGTGGCAACAGAGAAATGTTTGGCTGCAAGAAACCTGCTACCCACA	459
Db	461	ACTATGTTTGGAGGAACAAAGGACAAATGTCTGTCTGTTCTCAGAAACGGTTTATCCACT	520
Qy	460	GAAAGGTATCACCCATATGCAACGCCATACCATTAAGAGCTGCTTCCAAATGCAAGCCACGGA	519
Db	521	GAGGAAGGTGACTGTGAATGAAGAAACCCCTTACCATTAAGAGTTGTTTCCAATGCTGTCATGGA	580
Qy	520	GCGCTGTAAATAGCCCTCCCAACTATTCGCCACATGAGGGGGCGCTTATATTTGAACAT	579
Db	581	GGGTGTATTACAGTCTCTTCCAAATTACATAGACACAGGGAAGAAACTCTACTGCAAAAC	640
Qy	580	CACCATATTTCAACTTATCAAGAGAGGAGGCACTTAAGCAAGCTTGAAGGTTGACCATGAA	639
Db	641	CACCATGTGCAATTCATCAAGAGAGGAGGCAATTTAAGCCAACTTGAAGGTTGACCAATGAG	700


```

; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 36088
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-36088

Query Match
Best Local Similarity 34.4%; Score 339.6; DB 41; Length 973;
Matches 439; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGGAGACACAGAAATGCATGCGATGTGACAGAGCTGTCTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 ATGGCATTTTGCAGGAGAACCCAGAGTGTATGGCTCGGACAAACGGTTTATCTGTT 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 GACAAATTACATGACAGATACAGATCTATCACAAAGCTTGTTCAGATGCCATCTGC 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 GATTAAGTTACCGCGGATACCGAGTGTTCACAAAGCTTGTTCAGATGCCATCTGC 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 AAGGCACTGTCAAGCTTCACTCAATTCCTTTGAGGAGTTCTATACCTAGACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 AAGGAACCCCTCAGCTGACACATCTCTTTGAGGAGTTCTTTACGCAAGCCA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CACTTTGATCAGCTCTTCAACAACTGGCAGTTTGATTAAGCTTTGAGGTACACCA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 CATTTTGACCACTGTCTTCAAGAACTGGAGGCTTGACAAAGCTTTGAGGACACCA 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 AAAAATGTAGAGCCAGAAACCCATTGACAGTGAAGAAACACAGGTAGCCAAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 AAAATTGCCAAGCCAGAAATTTTGA--AGAGAAACCTGCACAGCCAAAGTCTCA 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGCATGTTTGGTGAGCAAGAGAAATGTTTGGCTGCAAGAAACCTGCTACCCACA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 463 AGTATGTTTGGTGAGCAAGAGAAATGCTGCTGTGTCAGAAACGGTATCCACAT 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GAAAGGTATCAGCCATGAGCCATCATTAAGAGCTGCTTCCATGACGACGCA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 GAGAAGTTACTGTGAATGGAACCTCTTACATTAAGAGTTGTTTAAATGCTGCCATGCA 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GCGTGTATAAAGCCCTTCCAACTATACCGCATGAGGGGCGCTTATATTGTAACAT 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 GGGTGTATATCAGTCTTCCAACTATACGACAGGAGGAAACCTTACTCATAACAC 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 CACCATATTCACATTTATCAAGAGAGGCAACTTAAAGCAAGCTTGAAGGTGACCATGAA 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 CACCATGTCCATTTGATCAAGAGAGGCAATTTAAACCAACTTGAAGGTGACCATGAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 ATGAATTCACGACAAACAGAGGATTACTGCAGAGTCAATACAG 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 703 AAGAGTGCAGCTAATGGAATAATCAATGATGGAAGATTTCGCCAG 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-60-312-544-1609
; Sequence 1609, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerlon, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
```

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; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 1609
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(756)
; OTHER INFORMATION: Clone ID: 700888137_FLI
US-60-312-544-1609

Query Match
Best Local Similarity 34.4%; Score 339.6; DB 75; Length 973;
Matches 439; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGGAGACACACAGAAATGCATGCGATGTGACAGAGCTGTCTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 ATGGCATTTTGCAGGAGAACCCAGAGTGTATGGCTCGGACAAACGGTTTATCTGTT 225
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 160 GACAAATTACATGACAGATACAGATCTATCACAAAGCTTGTTCAGATGCCATCTGC 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 GATTAAGTTACCGCGGATACCGAGTGTTCACAAAGCTTGTTCAGATGCCATCTGC 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 220 AAGGCACTGTCAAGCTTCACTCAATTCCTTTGAGGAGTTCTATACCTAGACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 286 AAGGAACCCCTCAGCTGACACATCTCTTTGAGGAGTTCTTTACGCAAGCCA 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 280 CACTTTGATCAGCTCTTCAACAACTGGCAGTTTGATTAAGCTTTGAGGTACACCA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 346 CATTTTGACCACTGTCTTCAAGAACTGGAGGCTTGACAAAGCTTTGAGGACACCA 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 340 AAAAATGTAGAGCCAGAAACCCATTGACAGTGAAGAAACACAGGTAGCCAAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 406 AAAATTGCCAAGCCAGAAATTTTGA--AGAGAAACCTGCACAGCCAAAGTCTCA 462
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 400 AGCATGTTTGGTGAGCAAGAGAAATGTTTGGCTGCAAGAAACCTGCTACCCACA 459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 463 AGTATGTTTGGTGAGCAAGAGAAATGCTGCTGTGTCAGAAACGGTATCCACAT 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 460 GAAAGGTATCAGCCATGAGCCATCATTAAGAGCTGCTTCCATGACGACGCA 519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 GAGAAGTTACTGTGAATGGAACCTCTTACATTAAGAGTTGTTTAAATGCTGCCATGCA 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 520 GCGTGTATAAAGCCCTTCCAACTATACCGCATGAGGGGCGCTTATATTGTAACAT 579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 583 GGGTGTATATCAGTCTTCCAACTATACGACAGGAGGAAACCTTACTCATAACAC 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 580 CACCATATTCACATTTATCAAGAGAGGCAACTTAAAGCAAGCTTGAAGGTGACCATGAA 639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 643 CACCATGTCCATTTGATCAAGAGAGGCAATTTAAACCAACTTGAAGGTGACCATGAG 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 640 ATGAATTCACGACAAACAGAGGATTACTGCAGAGTCAATACAG 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 703 AAGAGTGCAGCTAATGGAATAATCAATGATGGAAGATTTCGCCAG 748
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-928-412-1617
; Sequence 2276, Application US/09654617
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Annotated Plant Genes
; FILE REFERENCE: 38-21(15097)D
; CURRENT APPLICATION NUMBER: US/09/654,617
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 463173
; SEQ ID NO 2276
; LENGTH: 1006
; TYPE: DNA
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ORGANISM: Glycine max
US-09-654-617-2276

Query Match 34.3%; Score 338.6; DB 25; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 159
DB ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 235
QY 160 GACAAATTAATGATGATTAACAGATATATCACAAGCTTGTTCATGCTCATCTGC 219
DB GATTAAGTTGACCGGATTAACCGGATTTCCACAAGCTTGTTCATGCTCATCTGC 295
QY 220 AAGGCACTGTGATGCTTGCAGCACTATCAATTCCTTTGAGGAGTTCTATCTGATAGACA 279
DB AAGGAACCTCTCAAGCTGAGCACTACACTCTTTTGAAGGAGTTCTTACTGAGGACA 355
QY 280 CACTTTGATCAGCTCTTCAAAACAACCTGCGAGTTTGGATTAACCTTTGAAGTACACA 339
DB CACTTTGATCAGCTCTTCAAAACAACCTGCGAGTTTGGATTAACCTTTGAAGTACACA 415
QY 340 AAAAATGTGAAGCCACAGAAACCATTTGACATGAGAAACACAGTACCAAGTACA 399
DB AAAATGTGTAAACCAAGAAACCATTTGACATGAGAAACACAGTACCAAGTACA 472
QY 400 AGCATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCAACA 459
DB AGTATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCAACA 532
QY 460 GAAAAGTATACGCAATGCGACGCTTACCATTAAGAGTCTTCAATGACGACGACA 519
DB GAAAAGTATACGCAATGCGACGCTTACCATTAAGAGTCTTCAATGACGACGACA 592
QY 520 GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGCGCTTATATGTAACAT 579
DB GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGCGCTTATATGTAACAT 652
QY 580 CACCATATTCACCTTATCAAGAGAGGAGCACTTAAGCAAGCTTGAGGTCGACATGAA 639
DB CACCAGTCCACACTGATCAAGAGAGGCAATTTAAGCCAACTTGAGACGTCACATGAG 712
QY 640 ATGAATTCACGA 652
DB 713 AAGAGTCAACTA 725

RESULT 14
US-09-684-016-2276
Sequence 2276, Application US/09684016
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Annotated Plant Genes
FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684, 016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/654, 617
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 2276
LENGTH: 1006
TYPE: DNA
ORGANISM: Glycine max
US-09-684-016-2276

Query Match 34.3%; Score 338.6; DB 27; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 159
DB ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 159

DB 176 ATGGCAATTTGCGAGAACACACAGAAATGATGCGCTGTGACAAACCGTTATCTGTT 235
QY 160 GACAAATTAATGATGATTAACAGATATATCACAAGCTTGTTCATGCTCATCTGC 219
DB GATTAAGTTGACCGGATTAACCGGATTTCCACAAGCTTGTTCATGCTCATCTGC 295
QY 220 AAGGCACTGTGATGCTTGCAGCACTATCAATTCCTTTGAGGAGTTCTATCTGATAGACA 279
DB AAGGAACCTCTCAAGCTGAGCACTACACTCTTTTGAAGGAGTTCTTACTGAGGACA 355
QY 280 CACTTTGATCAGCTCTTCAAAACAACCTGCGAGTTTGGATTAACCTTTGAAGTACACA 339
DB CACTTTGATCAGCTCTTCAAAACAACCTGCGAGTTTGGATTAACCTTTGAAGTACACA 415
QY 340 AAAAATGTGAAGCCACAGAAACCATTTGACATGAGAAACACAGTACCAAGTACA 399
DB AAAATGTGTAAACCAAGAAACCATTTGACATGAGAAACACAGTACCAAGTACA 472
QY 400 AGCATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCAACA 459
DB AGTATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCAACA 532
QY 460 GAAAAGTATACGCAATGCGACGCTTACCATTAAGAGTCTTCAATGACGACGACA 519
DB GAAAAGTATACGCAATGCGACGCTTACCATTAAGAGTCTTCAATGACGACGACA 592
QY 520 GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGCGCTTATATGTAACAT 579
DB GCGTGTATTAAGCCCTTCAACTATACCGCATAGAGGGCGCTTATATGTAACAT 652
QY 580 CACCATATTCACCTTATCAAGAGAGGAGCACTTAAGCAAGCTTGAGGTCGACATGAA 639
DB CACCAGTCCACACTGATCAAGAGAGGCAATTTAAGCCAACTTGAGACGTCACATGAG 712
QY 640 ATGAATTCACGA 652
DB 713 AAGAGTCAACTA 725

RESULT 15
US-09-733-089-12353
Sequence 12353, Application US/09733089
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Lutfiyya, Linda L.
APPLICANT: McIninch, James
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
FILE REFERENCE: 38-21(15300)D
CURRENT APPLICATION NUMBER: US/09/733, 089
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/474, 435
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 09/654, 617
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 09/620, 392
NUMBER OF SEQ ID NOS: 24143
SEQ ID NO 12353
LENGTH: 1006
TYPE: DNA
ORGANISM: Glycine max
US-09-733-089-12353

Query Match 34.3%; Score 338.6; DB 29; Length 1006;
Best Local Similarity 77.0%; Pred. No. 2.7e-73;
Matches 426; Conservative 0; Mismatches 124; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 159
DB ATGGCTTTTGCAGAGACACAGAAATGATGCGATGTGCAAGACTGTCTATCTGTT 159

Db 176 ATGCGATTGCGAGAACACAGAAAGTGTATGGCCTGTGACAAAACGTTATCTGTT 235

QY 160 GACCAATTAACTGCAGATACAGAAATCTATACAAAGCTTTGTTGAGATGCCATCATGCG 219

Db 236 GATTAAGTTGACCGGAGATTAACGAGTTTTCACAAAAGCTTGCTTCAGATGCCATCATGCG 295

QY 220 AAGGCGACTGTACAGCTTGCGCACTACAAATTCCTTTGAGGAGTTCTATCTGTAGACCA 279

Db 296 AAAGGAAACCCCTGACCTGAGCACTACAACTCTTTGAGGAGTTCTTACTGTGACAGCCA 355

QY 280 CACTTGTGATCAGCTCTTCACAACTGCGCATTTGGATAAAAGCTTTGAGGTACACCA 339

Db 356 CACTTTGACCACTGTTCACAAAGACTGTAGTCTTGACAAAAGCTTGCAGAGGACACCA 415

QY 340 AAAAATGTGAAAGCCACAGAAACCCATTTGACAGTGAAGAAACACAGGTAGCCAAAGTGACA 399

Db 416 AAAATTTGCTAAACCAAGAAAACCGGGGA--AGAGAAACCTGCAGACCAACAAAGTCTCA 472

QY 400 AGCATGTTTGGTGGACAAAGAGAAATGTTTGGCTGCAAGAAAAGTGTCTACCCACA 459

Db 473 AGTATGTTTGGTGGAACTAGAGATAATGTGCCGGTTGTCAAGAAAACAGTGTATCCACT 532

QY 460 GAAAGGTATCAGCAATGCGCAGCCATACATTAAGAGCTGCTCCATGCAAGCCACGGA 519

Db 533 GAAAAGTTACTGTGATGGAACCTCTTATCAAGAGTTGTTCAATGCACTCATGGA 592

QY 520 GGCTGTGTAATAAGCCCTTCACACTATACCGCACATGAGGGCGCTTATATTGTAAACAT 579

Db 593 GGGTGTGTTATTAAGTCCCTCCAACTACATTGCACAGAGGCAAACTCTACTGCCAAGCAC 652

QY 580 CACCATATTCAACTTATCAGAGAGAGGCAACTTAAGCAAGCTTGAGGGTGCACATGAA 639

Db 653 CACCAAGTCCCAAGTATCAAGAGAGGCAATTTAAGCCAATTGAAGTGCACATGAG 712

QY 640 ATGAATTCACGA 652

Db 713 AAGAGTGAACTA 725

Search completed: November 23, 2002, 00:30:07
Job time : 3191 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:18:28 ; Search time 61 Seconds
(without alignments)
6967.572 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
Sequence: 1 gaatcgcgccgctcccaaa.....ctttagcgccgcaatlc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280232 seqs, 215092063 residues

Total number of hits satisfying chosen parameters: 560464

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	179.8	18.2	861	US-10-278-173-83	Sequence 83, Appl
2	75	7.6	504	US-10-152-319A-579	Sequence 579, Appl
3	44.4	4.5	853	US-10-152-319A-2070	Sequence 2070, Ap
4	42.2	4.3	9515	US-10-240-453-182	Sequence 182, App
5	40.4	4.1	294	US-09-724-676-43076	Sequence 43076, A
6	40.4	4.1	334	US-09-724-676-43075	Sequence 43075, A
7	40.4	4.1	730	US-09-724-676-43072	Sequence 43072, A
8	40.4	4.1	732	US-09-724-676-43074	Sequence 43074, A
9	40.4	4.1	875	US-09-724-676-43069	Sequence 43069, A
10	40.4	4.1	877	US-09-724-676-43071	Sequence 43071, A
11	40.4	4.1	1141	US-09-724-676-43067	Sequence 43067, A
12	40.4	4.1	1165	US-09-724-676-43068	Sequence 43068, A
13	39.6	4.0	466	US-09-724-676-43059	Sequence 43059, A
14	39.6	4.0	506	US-09-724-676-43064	Sequence 43064, A
15	39.6	4.0	904	US-09-724-676-43066	Sequence 43066, A
16	39.6	4.0	1047	US-09-724-676-43065	Sequence 43065, A
17	39.6	4.0	1049	US-09-724-676-43063	Sequence 43063, A
18	39.6	4.0	1337	US-09-724-676-43065	Sequence 43065, A
19	39.6	4.0	11812	US-10-240-453-306	Sequence 306, App
20	39.6	4.0	12409	US-10-240-454-7	Sequence 7, Appl
21	39.6	3.9	20486	US-10-240-485-164	Sequence 164, App
22	38.6	3.9	9728	US-10-257-166-174	Sequence 174, App
23	38.4	3.9	6121	US-10-240-485-31	Sequence 31, Appl
24	38.2	3.9	6391	US-10-240-453-11	Sequence 11, Appl
25	38.2	3.8	17848	US-10-240-453-37	Sequence 37, Appl
26	38	3.8	17848	US-10-240-453-37	Sequence 37, Appl

27	38	3.8	17848	6	US-10-257-166-57	Sequence 57, Appl
28	37.6	3.8	1218	6	US-10-092-411A-2422	Sequence 2422, Ap
29	37.4	3.8	14924	6	US-10-240-452-21	Sequence 21, Appl
30	36.8	3.7	5544	6	US-10-240-485-174	Sequence 174, App
31	36.8	3.7	6298	6	US-10-240-453-67	Sequence 67, Appl
32	36.8	3.7	7025	6	US-10-240-454-46	Sequence 46, Appl
33	36.8	3.7	7025	6	US-10-257-166-142	Sequence 142, App
34	36.8	3.7	8866	6	US-10-240-453-154	Sequence 154, App
35	36.8	3.7	15479	6	US-10-257-166-45	Sequence 45, Appl
36	36.6	3.7	11996	6	US-10-240-456-45	Sequence 45, Appl
37	36.6	3.7	13123	6	US-10-240-452-64	Sequence 64, Appl
38	36.4	3.7	387	5	US-09-513-999C-1611	Sequence 1611, Ap
39	36.4	3.7	482	5	US-09-513-999C-11929	Sequence 11929, A
40	36.4	3.7	754	5	US-09-724-676-13711	Sequence 13711, A
41	36.4	3.7	904	5	US-09-724-676-13711	Sequence 13711, A
42	36.4	3.7	6018	6	US-10-240-453-103	Sequence 103, App
43	36.4	3.7	10467	6	US-10-240-453-328	Sequence 328, App
44	36.4	3.7	14551	6	US-10-240-485-137	Sequence 137, App
45	36	3.6	284	5	US-09-513-999C-27884	Sequence 27884, A

ALIGNMENTS

```
RESULT 1
US-10-278-173-83
: Sequence 83, Application US/10278173
: GENERAL INFORMATION:
: APPLICANT: Jiang, Cai-Zhong
: APPLICANT: Brown, Pierre
: APPLICANT: Riechmann, Jose-Luis
: APPLICANT: Pineda, Omaira
: APPLICANT: Zhang, James
: APPLICANT: Yu, Guo-Liang
: APPLICANT: Pillgrim, Marsha
: APPLICANT: Keddle, James
: APPLICANT: Heard, Jacqueline
: APPLICANT: Reuber, Lynne
: APPLICANT: Ratcliffe, Oliver
: APPLICANT: Adam, Luc
: APPLICANT: Samaha, Raymond
: TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
: FILE REFERENCE: M81-009
: CURRENT APPLICATION NUMBER: US/10/278,173
: CURRENT FILING DATE: 2002-10-21
: PRIOR APPLICATION NUMBER: US/09/533,392
: PRIOR FILING DATE: 2000-03-22
: PRIOR APPLICATION NUMBER: 60/125,814
: NUMBER OF SEQ ID NOS: 177
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 83
: LENGTH: 861
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: OTHER INFORMATION: G654
US-10-278-173-83

Query Match      18.2%   Score 179.8;   DB 6;   Length 861;
Best Local Similarity 58.6%   Pred. No. 4.2e-41;
Matches 352;   Conservative 0;   Mismatches 242;   Indels 7;   Gaps 2;

OY 100 ATGCGCTTTGAGGACACACAGCAATGATGCGATGTCAGCAAGCTGTCTATCTGCTT 159
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATGCTTTTACAGGACATCAACAGAAATGCAAGGCTTGTGGAAGACTGTTATGCTGTT 135
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 160 GACAAATTAACAGTGCAGTAACAGATCTATCAACAAAGCTTGTTCAGATGCCATCACTGC 219
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 GAGCTTCTCTGCTGATGAGGATGATGATCAACAGCTTGTCAATGACATCACTGC 195
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 220 AAGGCACTGTACAGCTTGGCACTACATTCCTTTAGGAGGATCTCATCTATCTAGACCA 279
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Db 196 AAAACGAGGCTTCAGCTGAGTAGTTCATCATCATGGAAGTGTGTTTGTACTGTAAAGCT 255
QY 280 CACTTGTGATCAGCTCTTCAACAACACTGGCAGCTTGGATAAAGCTTTGAAGTACACCA 339
Db 236 CATTGTGAGCAGCTCTTAAAGAGAGAGTGTGTGTTCACACGAAGACTTTCAGTCACTGCA 315
QY 340 AAAAATGTGAAGCCAGCAAAACCCATTGACAGTGAAGAAACCCAGAGTACCCAAAGTGA 399
Db 316 AAA-----TGGCTGACAAATCAACTCCTGAGCTGACAGAGAGCCCTAGCCGAGTTCCT 369
QY 400 AGCATGTTTGTGGAACAAGAGAGAAATGTTTGGCTCAAGAAACCTGTCTACACACA 459
Db 370 GGCAGGTTCTCTGTCGACACAGAGAAATGCGCCACTTGTAGTAAACCTGTGATCTTAT 429
QY 460 GAAAAGTATCAGCCATATGCAAGCCATACATTAAGAGCTGCTTCCAAATGCAAGCAGCA 519
Db 430 GAAAAGTATCAGCTGACAGAGAGAGATATCACAAGTCTCTTCAAGTGTACATGGA 489
QY 520 GCGTGTATTAATAGCCCTTTCACATATACCGCAGTGAAGGGCGCTTATTTGTTAAAT 579
Db 490 GGTGTCCTCAATTTTCACTTCAACTACGAGCTCTTGAAGAAATCTGTACTGCAAGAC 549
QY 580 CACCATATTCACATTAATCAGAGAGAGAGCAACTTAAGCAAGCTTGAGGGTGAACATGA 639
Db 550 CATTTCGCTCAGC-TCTTAAGGAGAGAGGAAATTACACCACTTATCAATCCGCTTCC 608
QY 640 ATGAATTCACGACACACAGAGAGTATCTGACAGATCATACACAGCCGACCAAGTTGAT 699
Db 609 ATCAAGCCTTCGAGCGCAGAGAGTCCGCCGCTGACAGAGAGCTCCGTTCTCTGAA 668
QY 700 T 700
Db 669 T 669

RESULT 2
US-10-152-319A-579/C
Sequence 579, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
PRIOR APPLICATION NUMBER: 2002-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 579

LENGTH: 504
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. AI008930
US-10-152-319A-579

Query Match 7.6%; Score 75; DB 6; Length 504;
Best Local Similarity 58.1%; Pred. No. 1e-11;
Matches 132; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 122 AGAATGATGGCATGTATGACAAAGACTGTCTATCTGTGACAAATTAAGTCAATACA 181
Db 432 AGACCTGTGACAGCCGCGCAAGAGAGACTGTGATCCCTATGAGAGCGGCTGTGACAGCAAGC 373
QY 182 GAATCTATCACAAGCTTTGTTTTCAGATGCAATGCAAGGCACTGTCAAGCTTGCA 241
Db 372 TCATTTCCACACACTCTTGTCTCTGTGCAAACTGTCACACCACTGCAAGCTGAGGCA 313
QY 242 ACTACAAATTCCTTTGAGGAGTTCTATATCTGTAGACCACTTTGATCAGCTCTTCAAC 301
Db 312 GTTACGCTGCATGACAGCGTGAATTTTACTGCAAACTCCTCAGCAGCTGTTTAA 253
QY 302 AACTGCGAGTTTGATTAAGCTTTGAGTACACCAAAATGTG 348
Db 252 GCAAGGCAACTACGATGAGGGGTTTGTGCTTAAACACACAGAGAG 206

RESULT 3
US-10-152-319A-2070
Sequence 2070, Application US/10152319A
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
PRIOR APPLICATION NUMBER: 2002-05-22
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 2070
LENGTH: 853
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_057144
US-10-152-319A-2070


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FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 43070
LENGTH: 294
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-43070

Query Match
Best Local Similarity 61.3%; Pred. No. 0.045; Length 294;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY      410 GTGGACAGAGAAGAAATGTTTTGCCTGCACAAGAAAAGTGTTCACCACAGAAAAAGTTAT 469
Db       99 GGGCGGGAGGGCAAAATGTGAGCCTGTGAANAAGACCGCTTACCATTGCACAGAAATCC 158
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      470 CAGCCAATGGCAGCCCATFACCATTAAGAGCTGCTTCCATGCAAGCCA 515
Db      159 AGTGCAATGGAAGAGATTGCCAACAGACGTGTTCACATGCAGCCA 204
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 6
US-09-724-676-43076
Sequence 43076, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 43076
LENGTH: 334
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-43076

Query Match
Best Local Similarity 61.3%; Score 40.4; DB 5; Length 334;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY      410 GTGACACAGAGAAATGTTTGGCTGCACAGAAAAGTGTATCCACAGAAAAGTAT 469
Db       99 GGGCGGGAGGGCAAAATGTGAGCCTGTGAANAAGACCGTGTACCATGCACAGAAATCC 158
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      470 CAGCCAATGGCAGCCCATFACCATTAAGAGCTGCTTCCATGCAAGCCA 515
Db      159 AGTGCAATGGAAGAGATTGCCAACAGACGTGTTCACATGCAGCCA 204
        ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-09-724-676-43075
Sequence 43075, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 43075
LENGTH: 730
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-676-43075

Query Match
Best Local Similarity 61.3%; Score 40.4; DB 5; Length 730;
Matches 61.3%; Pred. No. 0.06;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:05:53 ; Search time 2618 Seconds

(without alignments)
10983.030 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
Sequence: 1 gaatcgcgccgttcccaaa.....cttgcgcgcgcgcgaattc 988Scoring table: IDENTIFY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
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2: gb_hlg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
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41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	988	100.0	988	6	AR173368
2	984.8	99.7	988	6	E29450
3	953.8	96.5	957	8	AB023479
4	737.6	74.7	898	8	AF184109
5	587	59.4	615	8	AB079513
6	378	38.3	1036	8	AB079510
7	353	35.7	728	8	AF187105
8	332	33.6	573	6	AX412728
9	332	33.6	610	8	AF370569
10	331	33.5	886	8	AF085377
11	322.2	32.6	873	8	AY072143
12	309	31.3	904	8	AF197567
13	308.4	31.2	813	8	AF197568
14	300.4	30.4	897	8	AF049917
15	286.8	29.0	1015	6	AR123331
16	286.8	29.0	1015	6	E15767
17	269	27.2	930	8	AF135591
18	237.8	24.2	956	8	AF187103
19	236.2	23.9	912	8	AF187104
20	229.2	23.2	1563	8	AB079512
21	193.4	19.6	631	8	AY091249
22	193.4	19.6	977	8	AY063924
23	193.4	19.6	991	8	AY084361
24	192.4	19.5	694	8	AF370574
25	180	18.2	848	8	AF443117
26	179.8	18.2	882	8	AFRNAATL2
27	174.8	17.7	948	8	AY094448
28	173.6	17.6	603	6	AX412775
29	173.6	17.6	603	8	AY122901
30	170	16.2	966	8	NFLIMDOM
31	157.6	16.0	960	8	AF116851
32	150.8	15.3	3229	8	AY059790
33	134.4	13.6	994	8	AF047353
34	121.6	12.3	1948	8	AB079511
35	115	11.6	130154	2	AC125482
36	114	11.5	1773	8	AF116849
37	110.2	11.2	1880	8	AF116849
38	105.8	10.7	133658	2	CNS08CNO
39	102.2	10.3	1140	8	ATLIMI
40	102.2	10.3	100746	8	AC005489
41	79.8	8.1	1439	8	HASF3DNA
42	79.6	8.1	473	11	G71367
43	78.2	7.9	1081	6	AX046338
44	78	7.9	1216	9	BC022888
45	78	7.9	2264	9	AK097519

ALIGNMENTS

RESULT 1
LOCUS AR173368 988 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6303847.
ACCESSION AR173368
VERSION AR173368.1 GI:11912859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 988)
AUTHORS Kawoka, A. and Ebinuma, H.
TITLE DNA encoding a transcription factor controlling phenylpropanoid biosynthesis pathway
JOURNAL Patent: US 6303847-A 1 16-OCT-2001;

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FEATURES
  source      Location/Qualifiers
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              /organism="unknown"
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ORIGIN
Query Match      100.0%; Score 988; DB 6; Length 988;
Best Local Similarity 100.0%; Pred. No. 2e-250;
Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCGCGCGCGTTCACAAACCAAGTGTCAACACAAAGAAAGGAAAGAGCCACAAG 60
  1 GAATTCGCGCGCGTTCACAAACCAAGTGTCAACACAAAGAAAGGAAAGAGCCACAAG 60
Db
QY 61 ACCATTTTGTCTCTGTAAACTGCTCGTATATAGCCATGGCTTTGCGAAGCACA 120
  61 ACCATTTTGTCTCTGTAAACTGCTCGTATATAGCCATGGCTTTGCGAAGCACA 120
Db
QY 121 CAGAAATGCATGGCATGTGCAAGACGTCTATCTGTGTCACAATTAACCTGCGATTAAC 180
  121 CAGAAATGCATGGCATGTGCAAGACGTCTATCTGTGTCACAATTAACCTGCGATTAAC 180
Db
QY 181 AGAATCTATCACAAGCTGTTTCAGATGCCATCTGCAAGGGCGACTGTCAAGCTTGGC 240
  181 AGAATCTATCACAAGCTGTTTCAGATGCCATCTGCAAGGGCGACTGTCAAGCTTGGC 240
Db
QY 241 AACTACAAATTCCTTTGAGGAGTTCTATAGTAGACACACTTTGATCAGCTCTTCAAA 300
  241 AACTACAAATTCCTTTGAGGAGTTCTATAGTAGAGACACACTTTGATCAGCTCTTCAAA 300
Db
QY 301 CAACACTGGCGATTGGTAAAGCTTTGAAGTACACCAAAAAATGTGAAGCCACAGAAA 360
  301 CAACACTGGCGATTGGTAAAGCTTTGAAGTACACCAAAAAATGTGAAGCCACAGAAA 360
Db
QY 361 CCCATTGACAGTGAAGAACCAAGTAGCCAAAGTGAAGCAAGCTTTGGTGGAGACAGA 420
  361 CCCATTGACAGTGAAGAACCAAGTAGCCAAAGTGAAGCAAGCTTTGGTGGAGACAGA 420
Db
QY 421 GAGAAATGTTTGGCTGCAAGAAAAGTCTACCCCAACAGAAAAGGTATCAGCCAAATGGC 480
  421 GAGAAATGTTTGGCTGCAAGAAAAGTCTACCCCAACAGAAAAGGTATCAGCCAAATGGC 480
Db
QY 481 AGCCATACCATTAAGAGCTCTTCATGAGCAGCGAGGCGTGTGAATTAAGCCCTTCC 540
  481 AGCCATACCATTAAGAGCTCTTCATGAGCAGCGAGGCGTGTGAATTAAGCCCTTCC 540
Db
QY 541 AACTATACCGCACATGAGGGGCGTTATATTTGAATCAATCACCATATTTCAACTTATCAAG 600
  541 AACTATACCGCACATGAGGGGCGTTATATTTGAATCAATCACCATATTTCAACTTATCAAG 600
Db
QY 601 GAGAAAGGCACTTAAGCAAGCTTGAAGGTGACCATGAATTAATTCACGACACACA 660
  601 GAGAAAGGCACTTAAGCAAGCTTGAAGGTGACCATGAATTAATTCACGACACACA 660
Db
QY 661 GGAGTTACTGACAGATCATACAGCGAGCAAGTGAATGATTCCTTATACCGCGCA 720
  661 GGAGTTACTGACAGATCATACAGCGAGCAAGTGAATGATTCCTTATACCGCGCA 720
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QY 721 TCATGATTAATACGATCTGCTGTAGTTGAAGATGAAGAGCGCTTCAGACGCTTCCATGA 780
  721 TCATGATTAATACGATCTGCTGTAGTTGAAGATGAAGAGCGCTTCAGACGCTTCCATGA 780
Db
QY 781 ATGCACTTGGCTTGGCCGACCGATTTTACTCTAATCTAGCTTCAATTAATTTGATGT 840
  781 ATGCACTTGGCTTGGCCGACCGATTTTACTCTAATCTAGCTTCAATTAATTTGATGT 840
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QY 841 TGAACTATATATGTAGCTTTGTGTAGATTTTGAACCTTTTGTGCTTGTCTTC 900
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QY 961 ATGCCAAATCTTTGAGCGCGCGCAATTC 988
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E29450
DEFINITION
Transcriptional factor regulating phenylpropanoid biosynthesis
pathway.
ACCESSION
E29450.1 GI:13021011
VERSION
JP 1999276181-A/1.
KEYWORDS
unidentified.
SOURCE
unidentified.
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 988)
AUTHORS
Akiyoshi, K. and Hiroyasu, E.
TITLE
Transcriptional factor regulating phenylpropanoid biosynthesis
PATENT: JP 1999276181-A 1 12-OCT-1999;
JOURNAL
NIPPON PAPER IND CO LTD
OS
Nicotiana tobaccum
PM
JP 1999276181-A/1
PD
12-OCT-1999
PE
01-APR-1998 JP 1998125171
PR
AKIYOSHI KAMAOKA, HIROYASU EBINUMA
PI
C12N15/09, A01H5/00, C12N5/10, C12P21/02, (C12N15/09, C12R1: 91),
PC
(C12N5/10, C12R1: 91), (C12P21/02, C12R1: 91), C12N15/00, C12N5/00,
PC
(C12N15/00, C12R1: 91), (C12N5/00, C12R1: 91)
CC
Key CDS FT FT FT
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Matches 986; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 61 ACCATTTTGTCTCTGTAAACTGCTCGTATATAGCCATGGCTTTGCGAAGCACA 120
  61 ACCATTTTGTCTCTGTAAACTGCTCGTATATAGCCATGGCTTTGCGAAGCACA 120
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QY 181 AGAATCTATCACAAGCTGTTTCAGATGCCATCTGCAAGGGCGACTGTCAAGCTTGGC 240
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QY 361 CCCATTGACAGTGAAGAACCAAGTAGCCAAAGTGAAGCAAGCTTTGCTGCGACAGACA 420
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OY	661	GGAGTTACTGCAAGATCATACACAGCCGACCAAGTTGATTTATCTTATCTTTACCGGA		720
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Db	901	ACTGTATTTAGTGAATGTTGAATGAGATTTGAATTAACATAGCTTTCTGTCCAGTGC		960
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LOCUS	AB023479	957 bp	mRNA	linear
DEFINITION	Nicotiana tabacum mRNA for transcription factor Ntlim1, complete cds.			PLN 24-MAY-2000
ACCESSION	AB023479			
KEYWORDS	AB023479.1 GI:5689135			
VERSIONS	transcription factor Ntlim1; Ntlim1.			
SOURCE	Nicotiana tabacum cell_line:SRL CDNA			to mRNA.
ORGANISM	Nicotiana tabacum			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.			
AUTHORS	Kawaoka, A., Kaechien, P., Yoshida, K., Endo, S., Yamada, K. and Ebihama, H.			
TITLE	Functional analysis of tobacco LIM protein Ntlim1 involved in lignin biosynthesis			
JOURNAL	Plant J. 22 (4), 289-301 (2000)			
MEDLINE	20307428			
REFERENCE	2 (bases 1 to 957)			
AUTHORS	Kawaoka, A. and Yoshida, K.			
TITLE	Direct Submission			
JOURNAL	Submitted (08-FEB-1999) Akiyoshi Kawaoka, Nippon Paper Industries, Central Research Laboratory; 5-21-1 Oji, Kita-ku, Tokyo 114-0002, Japan (E-mail:akiyoshi.kawaoka@nifty.ne.jp, Tel:81-3-3911-5106(fax 291), Fax:81-3-3914-3350)			
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ORIGIN										
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Oy	75	CTGTAAACTTGCTGTATTAGCATGGCTTTGCAGAACACACAGAAATCGATGC	134							
Db	61	CTGTAAACTTGCTGTATTAGCATGGCTTTGCAGAACACACAGAAATCGATGC	120							
Oy	135	ATGTGACAAGACTGTCTATCTGTGTGACAAATTAACTGCAGATAACAGAACTATCACAA	194							
Db	121	ATGTGACAAGACTGTCTATCTGTGTGACAAATTAACTGCAGATAACAGAACTATCACAA	180							
Oy	195	AGCTGTTTCAGATGCCATCCTGCAAGGCGACTGTCAAAGCTTGGCACTCAATCTCTT	254							
Db	181	AGCTGTTTCAGATGCCATCCTGCAAGGCGACTGTCAAAGCTTGGCACTCAATCTCTT	240							
Oy	255	TGAGGAGTTCTATCTGTAGACCCACACTTTGATGAGCTCTTCAACAACATGGCAGTTT	314							
Db	241	TGAGGAGTTCTATCTGTAGACCCACACTTTGATGAGCTCTTCAACAACATGGCAGTTT	300							
Oy	315	GGATAAAGCTTTGAAGGTACACCAAAAAATGTGAAGCCACAGAAACCATTGACATGA	374							
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Oy	375	GAACACACAGTAGCCCAAGTAGCAAGCATGTTGGTGGACACAGAGAAATGTTTTGG	434							
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Oy	435	CTGCAAGAAACTGCTCTACCCAAGAAAGGTATCAGCAATGGCAGCCATACCATTA	494							
Db	421	CTGCAAGAAACTGCTCTACCCAAGAAAGGTATCAGCAATGGCAGCCATACCATTA	480							
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Db	481	GAGCTGCTTCCAAATGCAGCCACGAGAGGCTGTGTAAAGAGCCCTTCAACTATACGCACA	540							
Oy	555	TGAGGGGCGCTTATTATTGTAAACATCACCATTCTCAACTTATCAAGAGAGAGGCACTT	614							
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Oy	615	AAGCAAGCTTGAGGGGTGACATGAATGAATCCACGACAAACACAGAGAGTTACTGCAGA	674							
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Oy	675	GTCATACACAGCCAGCAAGTTGATTTGATCTCTTATCTTACCGCATCATGTTATTAGSTA	734							
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Db	61	GACAAATTAACTGCGAGATAACAGAATCTATACCAAAGCTTGTTTAGATGCCATCCTGC	120
QY	220	AAGGGCACTGTCAAGCTTGGCAACACACAATTCCTTTGAGGAGAGTCTAATCTAGACCA	279
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QY	280	CACTTTGATCAGCTCTTAACAACAACCTGGCACATTGGATAAAAAGCTTGAAGGTACACCA	339
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REFERENCE
AUTHORS
1 Kumagai,D. and Kawai,S.
TITLE
LIM of woody plant
JOURNAL
Published only in Database (2002)
REFERENCE
2 (passes 1 to 615)
AUTHORS
Kumagai,D. and Kawai,S.
TITLE
Direct Submission
JOURNAL
Submitted (05-FEB-2002) Shinya Kawai, Tokyo University of
Agriculture and Technology, Department of applied Biological
Science: 3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan
(E-mail:skawai@cc.tuat.ac.jp, Tel:81-42-367-5862)
FEATURES
Location/Qualifiers
source
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/organism="Nicotiana tabacum"

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BASE COUNT      208 a      135 c      133 g      139 t
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Best Local Similarity 98.3%; Pred. No. 2,3e-144;
Matches 593; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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QY 157 GTTGACAAATTAACAGCATTAACAGATCTATCACAAAGCTTTGTTACAGATCCATCAC 216
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  61 GTTGACAAATTAACAGCATTAACAGATCTATCACAAAGCTTTGTTACAGATCCATCAC 120
QY 217 TCGAAGGGCAGCTGTCAGAGTTGGCAATCTAATCTCTTGGAGGAGTCTTATACGTAGA 276
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  181 CCACACTTTGATCAGCTCTTCAACAACACTGGCAGTTGGATTAAGAGCTTTGAAGGTAGA 240
QY 337 CCAAAAAATGTGAAGCCACAGAAACCATTTGACAGTGAAGAAACACAGTAGGACCAAGTG 396
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QY 397 ACAAGCATTTGGTGGTGAAGAGAAATGTTTGGTGGCAAGAAACCTGTCTACCA 456
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  421 GGAGGCTGTGTATTAAGCCCTTCCAACTATACCGACATGAGGGGGCTTATATTGTA 480
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Db
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DEFINITION    Populus kitakamiensis pl1lm1 mRNA for transcription factor LIM,
complete cds.
ACCESSION     AB079510
VERSION       AB079510.1 GI:18565111
KEYWORDS
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SOURCE
ORGANISM
  Populus kitakamiensis cDNA to mRNA.
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  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
  1
REFERENCE
  Kumagai,D. and Kawai,S.
  LIM protein of woody plant
  Published Only in Database (2002)
  2 (bases 1 to 1036)
AUTHORS
  Kumagai,D. and Kawai,S.
TITLE
  Direct Submission
JOURNAL
  Submitted (05-FEB-2002) Shinya Kawai, Tokyo University of
  Agriculture and Technology, Department of Applied Biological
  Science; 3-5-8 Saiwai-cho, Fuchu, Tokyo 183-8509, Japan
  (E-mail:skawai@cc.tuat.ac.jp, Tel:81-42-367-5862)
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  170 TCTGAAGCCATGCAATTTGTCAGGACACACCAAGATGATGTGATGACAAAGCTGTGC 229
QY 151 TATCTGGTTGACAAATTAACAGCATTAACAGATCTATCACAAAGCTTTGTCAGATGC 210
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  230 TATCTGGTTGACAAATTAACAGCATTAACAGCATTAACAGCTGTGTCGATGC 289
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  451 TACCCACAGAAAGGTATCAGCCATGGCAGCCATTAAGAGTGAAGCTTCCATGC 510
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  530 TATCCACTGAGAGAGTTTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 589
QY 511 AGCCAGGAGGCTGTGTATTAAGCCCTTCCAACTATACCGACATGAGGGGGCTTATAT 570
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  590 ATCCACGAGAGGATGTACAAATTAAGCCCATCAACTATGACATGAAGGTGGCCCTAC 649
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DB	710	GATATTGAGAGGACTCATGA	731
RESULT 7			
LOCUS	AF187105		
DEFINITION	Helianthus annuus LIM domain protein WLM1 (WLM1) mRNA, complete cds.		
ACCESSION	AF187105		
VERSION	AF187105.1	GI:5932435	
KEYWORDS			
SOURCE	Helianthus annuus.		
ORGANISM	Helianthus annuus		
REFERENCE	1	(bases 1 to 728)	
AUTHORS	Mundel, C., Baltz, R., Eliasson, A., Bronner, R., Gass, N., Krauter, R., Eyrard, J. L., and Steimetz, A.		
TITLE	A LIM domain protein from sunflower localizes to the cytoplasm and/or the nucleus in a wide variety of tissues and associates with the phragmoplast in dividing cells		
JOURNAL	Plant Mol. Biol. (1999) In press		
REFERENCE	2	(bases 1 to 728)	
AUTHORS	Eliasson, A., Gass, N., Hamman, P., and Steimetz, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-SEP-1999) Institute of Plant Molecular Biology, CNRS, 12 rue du General Zimmer, Strasbourg 67084, France		
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DB	61	GACAAATCACTGCTGATACAGAGGTGTTCACAAAGCTTCTTCAGATGCACACATTCG	120
QY	220	AAGGCACTGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGGATTCATTAATGAGACA	279
DB	121	AATGGACACACTAAAGCTCAGTACTACAAACCTTTTGAGGAGGTCTTTTATTCAGAGCA	180
QY	280	CACTTTGATGCGCTTCAACAAACAGGCGATTTGGATTAACCTTTGAAAGTACCA	339
DB	181	CACTTTGATGCGCTTCAACAAACAGGCGATTTGGATTAACCTTTGAAAGTACCA	240

QY	340	AAAAATGCTAAGCCACAGAAACCCATTGACAGTGGAGAAACACAGGTACCCAAAGTGACA	399
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ACCESSION	AX412728		
VERSION	AX412728.1	GI:21445186	
KEYWORDS			
SOURCE			
ORGANISM			
	thale cress.		
	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1		
AUTHORS	Glazebrook, J., Wang, X., Dangl, J. L., Eulgem, T. and Zhu, T.		
TITLE	Plant genes, the expression of which are altered by pathogen infection		
JOURNAL	Patent: WO 0222675-A 492 21-MAR-2002;		
	Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT		
	CHAPEL HILL, (US) ; Glazebrook, Jen (US) ; Wang, Xun (US) ; Dangl,		
	Jeffrey L. (US) ; Eulgem, Thomas (US)		
FEATURES			
source	1..573		
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Matches 407;	Conservative	0;	Mismatches 125;
		Indels	0;
		Gaps	0;
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Db	1	ATGGCGTTCGCGAGAACACCCAGAAATGCAATGAGCATGTGACAAACAGTTTATCTTGTG	60
QY	160	GACAAATTAAGTGCAGATTAACAGAAATCTATCAACAAAGCTTGTTCAGATGCCATCACTGC	219
Db	61	GACAAATTAAGTGCAGATTAACAGAAATCTATCAACAAAGCTTGTTCAGATGCCATCACTGC	120
QY	220	AAGGCACTGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGATTCTATCTGTAAGACCA	279
Db	121	AAGGCACTGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGATTCTCTACTGCGACAGCA	180
QY	280	CACTTGTATCAAGCTTGTCAACAAACCTGGCGATTGGATTAAGCTTTGAAGGTGACCA	339
Db	181	CATTTCGATCAAACTTCAAGAACTGGAAGTCTTGGAAAGGTTTGAAGGGGACACCA	240
QY	340	AAAAATGTAAGCCACAGAAACCCATTGACAGTGGAGAAACACAGGTAGCCAAAGTGACA	399
Db	241	AAGATTTGGGAACCTGATTAAGGCTTTTGGAGGAGAGAACTGCTGCGAACCAGATTTGCG	300
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VERSION	AY072143.1
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/note= results in a frameshift when compared with genomic
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QY	85	TGCTGTATTATAGCCATGGCTTTTTCAGAGAACACAGAAATGCATGTGACAAAG	144
DB	37	TGATCTCTTACAGAAATGGCTTGCAGAGAACACCCGAAATGATGATGTACAAA	96
QY	145	ACTGTCTATCTGGTTGACAAATTAACCTGCAGATTAACAGAAATCTATACAAAGCTTGTTC	204
DB	97	ACAGATTATCTTGTGCAGAAAGTTAACCCCGCATACCGGGTCTACACAAAGCTTGTTC	156
QY	205	AGATCCCATCTACGAAAGGCACTGTCAAGCTTGGCAACTCAATTCCTTTGAGGAGTT	264
DB	157	CGATCTCACCAATTCGAAAGAACTCTCAAGCTTACCAATTCACCTCTTGAAGAGTT	216
QY	265	CTATCTCTAGACCCACCTTTGATCAGCTCTTCAACAAACCTGGCAGTTGGATTAAGC	324
DB	217	CTCTACTGACAGCCCAATTTGCATTAACATTCACAGAACTGGAAGTCTTGACAAAGC	276
QY	325	TTTGAAGGTACACCAAAATATGTGAAGCCACAGAAACCATTTGACAGTGAAGAACACAG	384
DB	277	TTTGAAGGAGACACCAAGATTTGGAAACCTGTATAGCCTTTGGAGGAGAGAGACTGCT	336
QY	385	GTAGCCAAAGTGACAGCATTTTGTGTGAACAGAGAGAAATGTTTGGCTGCAGAAA	444
DB	337	GGAACCAAGTTTCGAAATATGTTGGTGAACACGAGGAAATGCGTGTGTCACACAA	396
QY	445	ACTGCTCTACCCACGAAAGGTATCAGCCCAATGGCAGCCCATACCATTAAGAGCTGCTC	504
DB	397	ACCGTGTATCCATTTGAAGAGGTAT-GGTGAATGGAACATTTGACACAAAGAGCTGCTC	455
QY	505	CAATCAGCCACGAGGCTGTGTATTAAGCCCTTCCAACTATACGCACATGAGGGCGC	564
DB	456	AAGTACACATGAGGCTGCACGATTAAGCCCTTGAATTCATATGCTCAGAGGGTAA	515
QY	565	TTATATTTAAACATCACCATATTCACCTTATCAAGAGAAAGGCACTTAACGAAGCTT	624
DB	516	CTATATTCAGACATCATCATATTCAGCTGATCAAGAGAAAGCACTTGAAGCAGCTC	575
QY	625	GAGGCTG 631	
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DEFINITION	Nicotiana tabacum pollen specific LIM domain protein 1a mRNA,		
ACCESSION	AF197567		
VERSION	AF197567.1		
KEYWORDS	GI:6467902		
SOURCE	Nicotiana tabacum.		
ORGANISM	Nicotiana tabacum		
REFERENCE	1 (bases 1 to 904)		
AUTHORS	Sweetman,J., Spurr,J., Eliasson,A., Gass,N., Steilmetz,A. and		
	Twell,D.		

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
Isolation and characterization of two pollen-specific LIM domain protein cDNAs from <i>Nicotiana tabacum</i> Sex. Plant Reprod. 12, 339-345 (2000)		2 (bases 1 to 904)	Sweetman, J. and Twell, D.	Direct Submission		
Submitted (21-OCT-1999) Biology, University of Leicester, University Road, Leicester, Leics LE1 7RH, UK				Location/Qualifiers		
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BASE COUNT	277 a	174 c	186 g	267 t		
ORIGIN						
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Best Local Similarity	73.2%	Pred. No. 7.4e-71;				
Matches 396; Conservative	0;	Mismatches 145;	Indels	0;	Gaps	0;
QY	100	ATGGCTTTTGGAGAACACACAGAAATGCATGCGATGTGACACAGCTGTCTATCTGTT	159			
Db	116	ATGAGCTTCGCGAGAACACGCAAAAGTGCATGCTTTGGACAAAACGGTATCTGGTG	175			
QY	160	GACAAATTAATCTGCAGATPAACAGAAATCTATCAACAAGCTTTGTTAGATGCCATCTGC	219			
Db	176	GATCGCTTTGGTGGTGAATTAATGCAATTTATCAAGAGCTTGCTTTAGGTGCTACCACTGC	235			
QY	220	AAGGCACTGTCACACTTGGCAACTACAAATTCCTTGAAGGGAGTCTTACTGTAGACA	279			
Db	236	AAAATGCTCTCAACTCAGTAATTTCAACTCTTTGAGGGGTAATTTACTGTAGGCT	295			
QY	280	CACCTTGATCAGCTCTTCAACCAACTGCGACATTTGATATAAGCTTTGAAGGTACACA	339			
Db	296	CACCTTGATCAGCTTTTAAAGAACTGCGACTTTGGACAAAGTTTGAAGAACTCGC	355			
QY	340	AAAAATGTGAAGCCACAGAAACCCATTTGACAGTGAAGAAACACAGCTAGGCCAAGTGACA	399			
Db	356	AAAGTCACAAAGCCAGAAAAACCTGTGACACGAAATGTGAGGGGAGCAAAAGTCTCA	415			
QY	400	AGCATGTTTGGTGGGAACAAGAGAAATGTTTGGCTGCAAGAAAACTGTCTACCCACA	459			
Db	416	AGTTATTTTGGCAGCGACAGAGGAAAAATGTGGGCTGCACTAAAACTGTATCCGATT	475			
QY	460	GAAGAAGTATCAGCAATGCGACGCGCATACCTTAAGAGCTGTTCCATATGACGCACACA	519			
Db	476	GAGAGGTAAGTGTATACAGGAACAGCATATCCATTAAGGCTTGCCTTAATATGACGATGGA	535			
QY	520	GAGCTGTATTAAGCCCTTCCTCAACTATACCCGACATGAGGGGGCGCTTATATTGTAACAT	579			
Db	536	GAGCTGTACATTAAGCCCATCAATTAATTAATGACATGAAGAAAGGCTTATTGCAAGCA	595			
QY	580	CACCATTTTCAACTTATCAAGGAGAAAGGCAACTTAAGCAGCTTGAGGGGTACCATGAA	639			
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Db	656	A 656				

[illegible]

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	OY	511	AGCAGGAGGAGCGTGTTAATAAGCCCTTCACACTATATACGCACATGAGGGGGCTTATAT	570
	DB	514	AGCATATGAGAGGCGTGTACATTAAGCCCATTAATATACATTGCAATGAGGAAGGCTTAT	573
	OY	571	TGTAACAATCACCATATYTCACTTATCAAGAGAAGGCCAACCTTAAGCAAGCTTGAGGAT	630
	DB	574	TGCAGACACCACCATATTCACGCTTCAAGAGAAAAGCAATTAACAGCAGTTAGTCT	633
	OY	631	GACCATGAAN 640 	
	DB	634	GACCATGAAN 643	
	RESULT 14			
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	DEFINITION	Petunia x hybrida PGPS/D1 (PGPS/D1) mRNA, complete cds.		
	ACCESSION	AF049917		
	VERSION	AF049917.1 GI:4105771		
	KEYWORDS			
	SOURCE	Petunia x hybrida. Petunia x hybrida Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Petunia. 1 (bases 1 to 897) Guyon,V.N., Astwood,J.D., Garner,E.C., Dunker,A.K. and Taylor,L.P. Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia Plant Physiol. 123 (2), 699-710 (2000)		
	REFERENCE			
	AUTHORS			
	TITLE			
	JOURNAL			
	MEDLINE			
	PUBMED	10859200		
	REFERENCE	2 (bases 1 to 897) Guyon,V., Astwood,J.D. and Taylor,L.P. Direct Submission Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA		
	FEATURES			
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	Query Match	30.4%; Score 300.4; DB 8; Length 897;		
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	Matches 394;	Conservative 0; Mismatches 156; Indels 0; Gaps 0;		
	OY	90 GTATATAGCCATGGCTTTTGAGAGAACACAGAAATGCATGCGATGTGACAAGACTGT	149	

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:04:58 ; Search time 255 Seconds

(without alignments)
8725.390 Million cell updates/sec

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Perfect score: 988

Sequence: 1 gaattcgcgccgtcccaaa.....cttgcgcgcgcgaattc 988

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336.4	34.0	983	21	AAC55884
2	334.2	33.8	956	21	AAC49742
3	332	33.6	969	21	AAC33426
4	331	33.5	886	21	AAC35197
5	295.4	29.9	744	24	ABQ65462
6	286.8	29.0	1015	19	AAV23830
7	284.8	28.8	830	21	AAC46607
8	284.2	28.8	1079	21	AAC51693
9	249.8	25.3	1116	21	AAC56321

10	224.6	22.7	672	21	AAC43077	Arabidopsis thalia
11	220.4	22.3	996	21	AAA31931	Plant microstelli
12	193.4	19.6	391	21	AAC36032	Arabidopsis thalia
13	190	19.2	418	21	AAA31779	Plant microstelli
14	186.6	18.9	521	21	AAC52052	Arabidopsis thalia
15	183.8	18.6	585	21	AAC56306	Pinus radiata tran
16	183.2	18.5	418	21	AAA31905	Plant microstelli
17	182.6	18.5	1196	21	AAC56302	Pinus radiata tran
18	174.8	17.7	835	21	AAC42582	Arabidopsis thalia
19	172.8	17.5	302	21	AAA31982	Plant microstelli
20	169.8	17.2	791	21	AAC42419	Arabidopsis thalia
21	167.8	17.0	338	21	AAC55893	Eucalyptus grandis
22	167.8	17.0	338	21	AAA31913	Plant microstelli
23	162.2	16.4	460	21	AAC56949	Pinus radiata tran
24	160.4	16.2	478	21	AAC55950	Eucalyptus grandis
25	158.8	16.1	764	21	AAC55952	Eucalyptus grandis
26	155	15.7	441	21	AAA31676	Plant microstelli
27	148.4	15.0	347	21	AAC57048	Pinus radiata tran
28	148.2	15.0	270	21	AAA31850	Plant microstelli
29	147.8	15.0	247	21	AAA31890	Plant microstelli
30	141.6	14.3	693	24	ABQ65714	Arabidopsis thalia
31	130	13.2	744	17	AAT29002	Parietaria allerge
32	129.2	13.1	322	21	AAC56921	Pinus radiata tran
33	126.2	12.8	787	17	AAT29008	Parietaria allerge
34	111	11.2	522	21	AAC56079	Eucalyptus grandis
35	108.8	11.0	845	17	AAT29009	Parietaria allerge
36	100.8	10.2	206	21	AAC57027	Pinus radiata tran
37	97.4	9.9	394	21	AAC56094	Eucalyptus grandis
38	97	9.8	458	21	AAC41015	Zea mays DNA fragm
39	90.8	9.2	748	17	AAT29001	Parietaria allerge
40	86.4	8.7	607	17	AAT29003	Parietaria allerge
41	85.8	8.7	639	17	AAT29000	Parietaria allerge
42	83.6	8.5	280	24	ABL74530	Corn tassal-derive
43	82	8.3	279	24	ABL75164	Pinus radiata tran
44	79.2	8.0	568	17	AAT29004	Parietaria allerge
45	79	8.0	402	21	AAA31486	Plant microstelli

ALIGNMENTS

RESULT 1	
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ID	14AC55884
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AC	AAC55884;
XX	XX
DT	25-JAN-2001 (first entry)
XX	XX
DE	Eucalyptus grandis transcription factor DNA sequence #15.
XX	XX
KW	Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW	poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW	basic helix-loop-helix zipper; homeotic; homeobox; MADS;
KW	homeodomain zipper; LIM domain; AP2; ERBS; zinc finger domain;
KW	type 2 Cys2His2; CCAAT box element; MYB; ss.
OS	Eucalyptus grandis.
XX	XX
PN	WO200053724-A2.
XX	XX
PD	14-SEP-2000.
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PF	09-MAR-2000; 2000WO-US06112.
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PA	18-AUG-1999; 99US-0149485.
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XX	(FLEET-) FLEETCHER CHALLENGE FORESTS LTD.
PI	Wood M, McGrath A, Shenk MA, Glenn M;
XX	XX

PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
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PR 26-OCT-1999; 99US-0161361.
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PR 29-OCT-1999; 99US-0162142.

Query Match 33.8%; Score 334.2; DB 21; Length 956;
Best Local Similarity 75.7%; Pred. No. 1.3e-85;
Matches 414; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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QY 265 CTATACGTGATAGCACTTTGATCAGCTCTTCAAACTGCACTTTGATGATTAAGC 324
DB 280 CTCTACTGACAGCACCATTTTCGATCAAACTTCAAGAGAACTGAGAGTTGAGAAAGC 339

QY 325 TTTCAGGTACACCAAAATGTGACAGCACAGAAACCCATTGACAGTGAAGAACACACAG 384
DB 340 TTTCAGAGGACACCAAGATGGGAAACCTGATAGGCTTTGGAGGGAGAGACCTGCT 399
QY 385 GTACCAAGTGAACACATGTTTGGTGAACAGAGAGAAATGTTTGGCTGCAAGAAA 444
DB 400 GGAACCAAGTTTGAATATGTTGGTGAACACAGAGAAATCGTTGGTGGACAAA 459
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RESULT 3
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AC AC33426;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 2994.

XX Hybridisation assay; genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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PR 04-OCT-1999; 99US-0157117.

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Query Match 33.5%; Score 331; DB 21; Length 886;
Best Local Similarity 75.3%; Pred. No. 1.1e-84;

Matches 412; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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RESULT 5
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DT 21-AUG-2002 (first entry)
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KW insecticide; antibiotic; ds.
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PA (ANY/) AN Y.
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PA (RAME/) RAMEKARA J G.
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PA (GARC/) GARCIA C A.
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PI Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
WP1: 2002-479224/51.
XX
PT New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
PT useful e.g. for preparing transgenic plants with increased resistance
PT or altered metabolism
XX
XX
XX Claim 1; SEQ ID NO 39; 40pp + Sequence Listing; English.
XX
XX The invention relates to nucleic acids (I) that hybridise under stringent
XX conditions to any of 999 sequences (AB065424-AB066422) or their
XX fragments. (II) are used to express the corresponding polypeptides (II) or
XX to produce genetically modified plant cells or transgenic plants, which
XX may have improved resistance to disease or stress, or altered
XX metabolic/biosynthetic pathways (for production of commercial,
XX nutritional or medicinal products), or generally any trait of interest,
XX or can be used to screen for biologically active agents (e.g. fungicides,
XX insecticides and antibiotics).
XX Note: The sequence data for this patent did not form part of the printed
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CC specification, but was obtained in electronic format directly from the
CC USPTO at seqdata.uspto.gov/sequence.html?docID=99909770149.
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SQ Sequence 744 BP; 234 A; 141 C; 164 G; 205 T; 0 other;

Query Match	29.9%	Score 295.4;	DB 24;	Length 744;
Best Local Similarity	75.3%	Pred. No. 1.6e-74;		
Matches 368;	Conservative	0;	Mismatches 121;	Indels 0;
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AC	AAV23830;		
XX	31-JUL-1998 (first entry)		
DJ	Cocton plant gene.		
XX	Cocton plant gene.		
DE	Cotton plant gene; SF3 gene; sunflower; transcription factor;		
KW	cotton fibre formation; ds.		
KM	Gossypium hirsutum.		
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PE	20-SEP-1996; 96JP-0250122.		
PR			
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PA (NISN) NISSHINO IND INC.
 XI
 PI Aotsuka S, Hasegawa O, Takenishi S, Uchimiya H,
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 WP1: 1998-195464/18.
 DR P-PSDB; AAW54022.

PT Transcription factor gene from cotton plants - used to modify the
 XX character of fibres, useful in the fibre, paper and food industries
 PS Claim 2; Page 13-14; 19pp: English.

Claim 2; Page 13-14; 19pp; English.

This sentence encodes a cotton plant protein. The encoded protein shows homology to sunflower SP2 and transcription factors. The protein is a transcription factor expressed in large amounts in fibre cells of cotton plants during cotton fibre formation. By modifying expression of the DNA it is possible to modify the character of the fibres to produce cotton plants useful in the fibre industry, the paper-manufacturing industry and the food industry.

Sequence 1015 BP; 330 A; 203 C; 202 G; 280 T; 0 other;

Query Match	29.0%;	Score 286.8;	DB 19;	Length 1015;
Best Local Similarity	71.4%;	Pred. No. 5.6e-72;		
Matches 394;	Conservative 0;	Mismatches 152;	Indels 6;	Gaps 1.

QY	102	GGCTTTTCGAGGAACCCACACAGAAATGCATGGCATGTGCACAAGACTGTATCTGTGTTGA	161
Db	139	GACATTTCCACAGGAACCTCAACAAAAATGGCAAAATGCAGACAGACTGTTATCTGGTGA	198
QY	162	CAAAATTAACCTGAGATTAACAGATCTATACAAAGCTTGTTTGCATGCCATCACTGCA	221
Db	199	TAAAGTTGACGGCTGATATATAGGTTTTTTCATAAAGCTTGCTCCGTTGCCACATTCGCA	258
QY	222	GGGCACTGCTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGATTCATATCTGTAGACACA	281
Db	259	GGGTACCTCAAGCTTTAGCACTACAACTCATTTGAAAGGGTGTCTATACGCAAGCCACA	318
QY	282	CTTTGATCAGCTCTTCAACAACACTGGCAGTTTGGATPAAAAGCTTTGAAGTACACCAA	341
Db	319	CTATGATCAACTCTTCAAGAGAACTGGCAGCTCTTGACAAGAGTTTGAAGGAACCCAA	378
QY	342	AAATGTGAAGCCACAGAAACCCATTTGACAGTGAAGAAACCCAGTACCACAACTGACAA	401
Db	379	GGTTGCTCAACCTGAAACACAAATCGATAGTGAAGAGTGCACATG-----AAAGTATGAA	432
QY	402	CATGTTTGGTGGAAACAAGAGAATCTTTTGGCTGCACAAGAAAATCTGTACCCACAGA	461
Db	433	CTCGTTTGGTGGACACAGAGAAAATGTGGGGCTGTCTTAAGACTGCTTATCCAAATTGA	492
QY	462	AAAGGTATCAGCCAAATGCGACGCCACTACATTAAGAGCTGCTTCCAAATGACGCCAGGAG	521
Db	493	GAGGGTACTGTGAATGGGACAATATATCCCAAGAGAGCTGCTCAAGTGTACCATTGAGG	552
QY	522	CTGTGTATTAAGCCCTTCCAACTATACCGCACATGAGGGCGCTTATATTGTAAACATCA	581
Db	553	GTTGACCACTTGGCCATCAAACTATTATAGACACATGAAGGTAAACTACTACGCAAAATCA	612
QY	582	CCATATTCACCTATTCAAAGGAAGGAGCAACTTAAGCAACTGTAGGGTGCACATGAAT	641
Db	613	CCATATTCACCTCTTTCAAAGGAAGGAAGAAACTACAGCCAACTGAGACCGAAGAGAA	672
QY	642	GAATTCACAGCAGC	653
Db	673	ACAAGCCGCCAC	684
RESULT 7			
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ID AAC46607 standard; DNA: 830 BP.			
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AC AAC46607:			

DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 50759.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM Protein identification; signal transduction pathway; metabolic;
KM pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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Query Match 28.8%; Score 284.8; DB 21; Length 830;
Best Local Similarity 69.4%; Pred. No. 1.9e-71;
Matches 404; Conservative 0; Mismatches 172; Indels 6; Gaps 1;
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Db 326 TGGGATAGAGA-----ATGCTACTAAAGTCTCAAGGCCCTTTTGGTGGACACAGAGAGAA 379
Qy 426 ATGTTTGGCTGCAAGAAAGTGTACCCAAACAGAGAAAGGTATACGCCAATGGCAGCC 485
Db 380 ATGTGTGGATGACAGACAGACAGTCTATCCAACTGAGAGGGTCACTGTTAATAACACTAT 439
Qy 486 ATACCATTAAGAGCTCTTCCAAATGAGCAGCCAGGAGCGTGTAAATTAAGCCCTTCCACTA 545
Db 440 GTACCAAGAGCTGCTTCAAGTGTCTGCAATGAGAGGTGACACCAATCAGCCCTTCACTA 499
Qy 546 TACCGACATGAGGGGCGCTTATATTGTAACATCACCATTATTCACATTATCAAGAGAGAA 605
Db 500 CATTGCGCAGCAGGGAGAGCTGTACTGCAACACACCACACATCCAGCTGATCAAGAGAGAA 559
Qy 606 GGGCACTTAAGCAAGCTTGAAGGTTGACCATGAATGAATTC 647
Db 560 GGGGAACCTTCAGCAGCTTGAGAAATGACCAAGAGACATC 601
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RESULT 8

AAC51693 standard; DNA; 1079 BP.

AAC51693:

18-OCT-2000 (first entry)

Zea mays DNA fragment SEQ ID NO: 69444.

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway; metabolic;
pathway; promoter; termination sequence; corn; ss.

Zea mays subsp. mays.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180.
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PR 25-MAR-1999; 99US-0126264.
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Best Local Similarity	70.7%	Prod. No.	3.2e-71				
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						Gaps	1

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Db	293	CGGCGATATGGCGACCTCCTTCACAGGGGACGACACCAGTAGTGACCGCTCGGACAAAGCTG	355
QY	149	TCATATCTGGTTGACAAATAATTAAGTCGAGATAAACAATCTATACAAAGCTTTGTTTCGAT	208
Db	353	TGTAACCTTGTGGACAGCTCACCGCGACAAACCGCATCTACACAAAGGCTGCTCCGCT	412
QY	209	GCCATCACTGCAAGGGCAGCTGTCAAGCTTGGCAACTCAATTCCTTTGAGGGAGTTCTAT	268
Db	413	GCCACCACTGCMAAGGGCACCTCTCAAGCTCGCAACTACAACTCCTTTCGAGGGAGTCTCT	472
QY	269	ACTGTACACACACTTTTGATCAGCTCTTTCAAACAACAAGTGCAGTTGGATTAAGACTTTCG	328
Db	473	ACTGACAGCCTCACTTTGACACAGCTGTTCACAGAGACAGGAGAGCTTGGACAAAGCTTCG	532
QY	329	AAGTACACCAAAAAATGTGAAGCCACAGAAACCATTGACAGTGAAGAAACACACAGSTAG	388
Db	533	AAGAACTCCCAAGGTTGTCAAGCGCAAAAAAGAAAGCTTGGGAATGAAATAGCTA-----	586
QY	389	CCAAAGTGCACAAAGCATTTTGGTGGTGAACAAGAGAAATGTTTTGGCTGCAAGAAAATCG	448
Db	587	CTAAAGTCTCAAGGGCTTTTGGCTGGCCACAGAGGAATGTGTTGGATGCAGCAAGACAG	646
QY	449	TCTACCCACAGAAAAAGGTATACAGCCAAAGTGCACGCCATTCATTAAGCTGTGCTCCAAAT	508
Db	647	TCTATCCAACTGAGAGGGGTACTAGTGTTAACAACACATATGTATACCAAGAGCTGTCTCAAGT	706
QY	509	GCAAGCCACGAGAGCGTGTGTATTAAGCCCTTCACAACTATACCGGACATGAGGGCGCTTAT	568
Db	707	GCTGCCATGAGAGGGGTGCACCATCAGCCCTTCTAACTACATTTGGCGACAGAGGGAGAGCTGT	766
QY	569	ATTGTAAACATCAACCATATTTCAACTTATCAAGGAGAAAGGCAACTTAAGCAAGCTTCAGG	628
Db	767	ACTGCAAGCCACCAACACATCCAGCTGATCAAGGAGAAAGGGAAGTCTCAGCCAGCTTGAGA	826
QY	629	GTCACCATGAAATGAATTC	647
Db	827	ATGACCAAGAGAAAGATTC	845

RESULT 9	
AAC56321	
ID	AAC56321 standard; DNA; 1116 BP.
XX	
AC	AAC56321;
XX	
DT	25-JAN-2001 (first entry)
XX	
DE	Pinus radiata transcription factor DNA sequence #121.
XX	
XX	
XX	Plant: transcription factor; gene expression: eucalyptus; pine; acacia
KW	poplar; sweetgum; teak; mangosay; bZIP; G-box binding factor;
KW	basic helix-loop-helix zipper; homeotic; homeodomain; homeobox;
KW	homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KW	type 2 Cys2His2; CCAAT box element; MYB; ss.
XX	
XX	
OS	Pinus radiata.
XX	
PN	WO200053724-A2.
XX	
XX	
14-SEP-2000.	
XX	

XX 09-MAR-2000; 2000WO-US06112.
PF
XX
XX 11-MAR-1999; 99US-0266513.
PR 18-AUG-1999; 99US-0149485.
PR
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX WPI: 2000-579369/54.
XX
XX
XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
PT -
XX Claim 1; Pages 162-163; 747pp; English.
XX

Sequence 1116 BP; 311 A; 202 C; 264 G; 339 T; 0 other;
CC
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC managony species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and ERBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
XX and MYB.

Query Match	25.3%	Score 249.8	DB 21	Length 1116
Best Local Similarity	67.2%	Pred. No. 2.4e-61		
Matches 353	Conservative	0	Mismatches 172	Indels 0
				Gaps 0

Qy	100	ATGCGTTTGGAGNACCACACAGAAATGCGATGGCATGTGACAAAGCTGTCTATCTGGTT	158
Db	202	ATGGCGCTTCGGCGGACACACCAGAACTGGCAAGGCAAGTGAAGAGGGCTATTATGGTT	261
Qy	160	GACAAATTAATCTGGAGATTAACAGAAATGATATCACCAAACTGTGTTTACATGCGATCACTGC	219
Db	262	GATCAATTTGACAGCTGATTAATCTGTTTTCACAAATCTGTTTCCGCTGCCATCACTGC	321
Qy	220	AAGGGCACTGTCAAGCTTTGGCACTACAAATTCCTTTGAGGGAGTTCTATCTAGTACCA	279
Db	322	AATGGAACCTTTAAAGCTTAGCAACTATTTCGTCGTTTGAAGGAGTCTATATTGCAAACT	381
Qy	280	CACTTTGATCAGCTCTTCAAAACAACCTGCGCAGTTTGGATTAAGCCTTTGAAGTACCA	339
Db	382	CATTTTTGCCACGCTGTTTAAGAGACAGGAAGTTTGGATTAAGATTGTTTGAAGCCATTCT	441
Qy	340	AAAATGTGAAGCCACAGAAACCCATTGACAGTATGAGAAACACAGGTAGCAAGTGTACA	399
Db	442	AGACATCTCAAGAAATTGACAGAGATGATGAGATGTAGAAACAGACACTAGTAAAGGTATCA	501
Qy	400	AGCATGTTTGGTGGAGACAAGAGAAATGTTTGGCTGCAGAAAGAACTGTCTACCCACA	459
Db	502	GCAATGTTTTCGGGTACACAGAGATTAATGTGTTGTCATGTGGAGAAACAGTACCCCATTT	561
Qy	460	GAAGAATATACGCCAATTGGCAGCCCATACCATTAAGAGCTGTCTTCCATGCTACCCACAGA	519
Db	562	GAGAGAGTGTGCTGTTGTATGGTACTCTTACCCAGCACAGCTTTTCAAGTCTCTCATGGT	621
Qy	520	GGCGTGTAAATACCCCTTCACATATATACCGACATGAGGGGGCTATATTTGAAACAT	579
Db	622	GGTTGTGTCAATCAGCCCTCAAAATTAATGTTGCTCATATGAAGGACAGGCTATATTGTAGCAT	681
Qy	580	CACCATATTCACTTATCAAGAGAGGAGCACTTAAGCAAGCTT	624

DB 682 CATAGCTCTCACTTTTATGGGAGAAAGTACTTCAGCCAGCTT 726

RESULT 10

AAC43077

ID AAC43077 standard; DNA; 672 BP.

XX AAC43077;

AC

XX 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37941.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EPI033405-A2.

XX

PD 06-SEP-2000.

XX

PE 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 06-MAY-1999; 99US-0132487.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142820.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

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PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149175.

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PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 23-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161820.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
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Query Match 22.7%; Score 224.6; DB 21; Length 672;
Best Local Similarity 64.7%; Pred. No. 3.3e-54;
Matches 408; Conservative 0; Mismatches 124; Indels 99; Gaps 1;

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QY 100 ATGGCTTTGCAGAACACAGAAATGATGGCATGTGACAAAGACTGTCTATCTGTG 159
DB 1 ATGGCTTTGCAGAACACACAGAAATGATGGCATGTGACAAAGACTGTCTATCTGTG 60
QY 160 GACAAATTAATCTCAGATACAGAAATCTATCACAAGCTTTGTTCAAGTCCATCACTGC 219
DB 61 GACAAGTTAACCGCGCATACCGGCTCTACCAACAAGCTTTGTTCCATCTCACCATTGC 120
QY 220 AAGGCACTGTCAAGCTTGGCAACTCAATTCCTTTGAGGAGTCTTATACTGTAGACCA 279
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DB 121 AAGGAACCTCAACCTTAGCAATTAACAACCTCTTGAAGAGATCTCTACTGACAGACCA 180
QY 280 CACCTTGATCAGCTCTTCAAAACAACTGCGAGTTGGTAAAGCTTGAAGT----- 333
DB 181 CATTTGCATCAAACTTCAAGAGAACTGGAAGCTTTGAGAAAAGCTTGAAGTAAATTA 240
QY 334 ----- 333
DB 241 CCAAAAACAGATCAAAATGTGAAAAAGTTTGTGAGTGAGGATTTCAATTTGCAATTATC 300
QY 334 -----ACACCAAAAATGTGAAGCCACAGAAA 360
DB 301 TATCTAAAGTTTGATTCATATATATGTACAGGACACACCAAAAGATTGGCAAACTCGATAGG 360
QY 361 CCCATTGACAGTGAAGAAACACAGGTAGCCAAAGTGACACAGCATGTTGGTGAACAAGA 420
DB 361 CTTTGGAGGAGAGAGACGCTGCTGGAACCAAACTTTCGAATATGTTTGGTGAACAGCA 420
QY 421 GAGAATGTTTTGGCTGCAGAGAAACTGTCTACCCACAGAAAGATATCAGCCCATGCGC 480
DB 421 GAGAATGCGTTGGTGGGACAAAACCGTATCAATTTGAAGGATATGCGTGAATGGA 480
QY 481 ACGCATACCATTAAGAGCTGCTTCCATGACGCCACGAGGCTGTGTATATAGCCCTTCC 540
DB 481 ACATTGTACCAAGAGAGCTGCTCAAGTGTACACATGAGAGCTCAGCATTAAGCCCTTCC 540
QY 541 AACTATACCCGACATGAGGCGGCTTATATGTAAACATCACATTTCAACTATACAG 600
DB 541 AATTACATAGCTCAGAGGAGTAACCTATATTTGCAAGCATCATATTTACAGTATCAG 600
QY 601 GAGAAGGCAACTTAAGCAAGCTTGAAGGAG 631
DB 601 GAGAAGGAAACTTGAGCAGACTCGAAGGAG 631
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RESULT 11
AAA31931
ID AAA31931 standard; DNA; 396 BP.
XX
AC AAA31931;
XX
DT 05-JUL-2000 (first entry)
XX
DE Plant microsatellite marker #892.
XX
KW Plant microsatellite sequence; core repeat sequence; detection; probe;
KW DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KW variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
OS
XX
PN WO967421-A1.
XX
PD 29-DEC-1999.
XX
PF 25-JUN-1999; 99WO-NZ00092.
XX
PR 25-JUN-1998; 98US-0105307.
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XX (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX Havukkala IU, Bloksberg LN, Glenn M;
XX WPI; 2000-116958/10.
XX
XX New plant microsatellite markers and associated flanking species for
XX the detection of polymorphic genetic markers -
XX Claim 1; Page 339; 392pp; English.

XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences

Db 801 T 801

RESULT 13
AAA31779
ID AAA31779 standard; DNA; 418 BP.

XX
AC AAA31779;
XX
DT 05-JUL-2000 (first entry)
XX
DE Plant microsatellite marker #740.
XX
XX Plant microsatellite sequence; core repeat sequence; detection; probe;
KM DNA polymorphism; genome mapping; physical mapping; fingerprinting;
KM variety identification; genetic variability evaluation; primer; ss.
XX
OS Eucalyptus grandis.
XX
XX WO967421-A1.
XX
XX 29-DEC-1999.
XX
XX 25-JUN-1999; 99WO-NZ00092.
XX
XX 25-JUN-1999; 98US-0105307.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Havukala IJ, Bloksberg LN, Glenn M;
PI
XX
XX WPI; 2000-116958/10.
XX
XX
XX New plant microsatellite markers and associated flanking species for
PT the detection of polymorphic genetic markers -
XX
XX Claim 1; Page 294-295; 392pp; English.
XX
XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences
CC and associated flanking species. The sequences comprise a central core
CC repeat sequence, especially selected from the sequences AAA32094-A32096
CC with left and right flanking sequences. The polymucleotide sequences
CC can be used in the detection of DNA polymorphisms, in genome mapping,
CC in physical mapping, in positional cloning of genes, in variety
CC identification and in evaluation of genetic variability within and
CC between plant tissues, populations, cultivars, species and species
CC groups. They may also be used to design hybridization probes for
CC oligonucleotide fingerprinting and library screening and to design
CC primers for microsatellite-primed PCR. Microsatellite markers are
CC useful to locate specific economically useful genes in plant genomes.
XX
XX Sequence 418 BP; 123 A; 105 C; 114 G; 76 T; 0 other;
SQ

Query Match 19.2%; Score 190; DB 21; length 418;
Best Local Similarity 73.7%; Pred. No. 2.3e-44;
Matches 255; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

QY 92 ATATAGCCATGGCTTTTGGAGAACACACAGAAATGCATGGATGACAGACGTCT 151
DB 34 AGAGAGAGATGCTTGGCGGAAACCCAGAGAGTGCGCTTGAGAAACAGTCT 93

QY 152 ATCTGGTGAACAATTAATGACAGATAACAGATCTATACAAAGCTTTTTCAGATGCC 211
DB 94 ATCTGGTGAACAAGCTGACAGCTGACATATGACATACCAAGGCTGCTTCAAGTCC 153

QY 212 ATCACTGCAAGGCGACTGTCAAGCTTGGCACTACATTCCTTTGAGGAGTTCTATCT 271
DB 154 ACCATTGCAACGCGACTCTCAAGCTTGGGAGACTATTAATTCATTGAAGAGCTCTTACT 213

QY 272 GTAGACCACTTGTGATGCTCTTCAACAAACCTGGAGCTTTGATTAAGCTTTGAAG 331
DB 214 GCGGGCGCATTTTGATTCAGCTCTTCAAGAGAACTGGCAGCCTCGAAAAAGCTTTGAAG 273

QY 332 GTACACCAAAAATGTGAAGCCACAGAAACCATTTGACAGTGAGAAACCAAGTAGCCA 391
DB 274 GACCCCCCAAGATTGCAAAAGCCGAGAAACCCGCTGCTGGAGAGACACTGCAAGGA-CCA 332

QY 392 AAGTGACAAAGCATGTTTGGTGGACAGACAGAGAAATGTTTGGCTG 437
DB 333 AAGCCTCCAGTATGTTCCGGGGGACCCGAGACACAAATGTGTGGATG 378

RESULT 14
AAC52052
ID AAC52052 standard; DNA; 521 BP.

XX
AC AAC52052;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 70282.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
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PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
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PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.

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 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
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 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
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AC
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DT 25-JAN-2001 (first entry)
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XX
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KW poplar; sweetgum; teak; mahogany; bzIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
KM homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
KM type 2 Cys2His2; CCAAT box element; MYB; ss.
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XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX
XX
DR WPI; 2000-579369/54.
XX
XX
PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
XX
XX
PS Claim 1; Pages 158-159; 747pp; English.
XX
XX
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bzIP, G-box family of G-box
CC binding factors, basic helix-loop-helix zipper, homeodomain zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
CC and MYB.
XX

SQ Sequence 585 BP; 174 A; 120 C; 136 G; 155 T; 0 other;
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Best Local Similarity 66.0%; Pred. No. 1.6e-42;
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	46.8	4.7	7218	1 US-08-232-463-14	Sequence 14, Appl
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7	37.8	3.8	1000	4 US-09-524-168-2	Sequence 2, Appl
8	37.6	3.8	1218	4 US-09-134-001C-2422	Sequence 2422, Ap
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ALIGNMENTS

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; Patent No. 6303847
; GENERAL INFORMATION:
; APPLICANT: KANAOKA, Akiyoshi
; APPLICANT: EBINUMA, Hiroyasu
; TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
; FILE REFERENCE: 4859-0027-0
; CURRENT APPLICATION NUMBER: US/09/282,146A
; EARLIER FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: JP 10-125171
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 988
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (100)..(702)
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; NAME/KEY: misc_feature
; LOCATION: (127)..(282)
; OTHER INFORMATION: LIM domain
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; LOCATION: (427)..(582)
; OTHER INFORMATION: LIM domain
; US-09-282-146-1

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Matches 988; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
 US-08-934-627B-1
 : Sequence 1, Application US/08934627B
 : Patent No. 6169174

GENERAL INFORMATION:
 : APPLICANT: OSAMU HASEGAWA
 : APPLICANT: SATOSHI AOTSUKA
 : APPLICANT: SOICHIRO TAKENISHI
 : APPLICANT: HIROFUMI UCHIMIYA
 : TITLE OF INVENTION: COTTON PLANT GENE
 : NUMBER OF SEQUENCES: 6
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Jones & Askew, LLP
 : STREET: 3424 Peachtree Road, N.E., 2400 Monarch Tower
 : CITY: Atlanta
 : STATE: Georgia
 : COUNTRY: USA

: ZIP: 30326
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentlin
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/934,627B
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Roger T. Frost
 : REGISTRATION NUMBER: 22,176
 : REFERENCE/DOCKET NUMBER: 20111-0010
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (404) 949-2400
 : TELEFAX: (404) 949-2499
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1015
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA to mRNA
 : ORIGINAL SOURCE:
 : ORGANISM: Gossypium hirsutum L.
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 134..757
 : US-08-934-627B-1

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 QY 522 CTGTATTAAGCCCTTCAACATATACCGCATGAGGCGGCTGTATATGTTAAATCA 581
 Db 553 GTGACCATTAAGCCATCAAACTATATAGCAATGAAGTAACTCTACGCAAACTCA 612
 QY 582 CCATATTCATTAAGAGGAGGCAACTTAAGCAAGCTTGAAGGTTGAGGTTACCAAT 641
 Db 613 CCATATCCAACTCTCAAGGAGAAAGAACTACAGCAACTGAGACCGAAGAGAGAA 672

APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991.677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 2251
TYPE: DNA
ORGANISM: Pinus taeda
US-08-991-677-11

Query Match 4.2%; Score 41.8; DB 4; Length 2251;
Best Local Similarity 55.0%; Pred. No. 0.0063;
Matches 82; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 824 TTCAATTAATTTGATGTTGAACATATATATGCTAGCTTTTGTGTGATTTTGGACCT 883
DB 282 TTGTGTTATTTTGAAGTTTATATAATTTTGTATATATTTTAAATAGTTAGCT 223
QY 884 TTGTTGCTTGTGCTTCTTCTGATATGATGATGTTGAATGAGTTGAATATATACATGG 943
DB 222 TATTATTTATTAATCTATTTTAAATTTTGTGAGAGAGTTGTGATGAAGAAGTTGTGA 163
QY 944 TTTTGCTGTCCAGTCATGCAATCTTT 972
DB 162 TTAAAGTGTATGTTGAAGAATTTCTTT 134

RESULT 6
US-08-691-814B-3
Sequence 3, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasello, Catherine
APPLICANT: Bassel, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
NUMBER OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691.814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3846 base pairs

TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 76..858
US-08-691-814B-3

Query Match 4.0%; Score 40; DB 2; Length 3846;
Best Local Similarity 53.1%; Pred. No. 0.03; DB 2; Length 3846;
Matches 85; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 124 AATGCGATGCGATGTGACAGACTGTCTATCTGTTGACAAATTAATGACAGATAACAGA 183
DB 85 AACTGCCGCCGCTGGCGGCAAGATGCTATCCACAGGAGAAAGTGAAGTGTGATTAAG 144
QY 184 ATCTATCACAAGCTTTGTTAGATGCCATGCACTGCAAGGCACTGTCAAGCTTGGCAAC 243
DB 145 TTCTGGCATTAAGCATGCTTCCATTTGCCAGACTGCAAGATGACACTGAACATGAAAGAAC 204
QY 244 TACAATTCCTTGGAGGAGGAGTTCTATCTGTAAGACCAACT 283
DB 205 TACAAGGCTTACGAGAGAGACCTTACTGCAACGCACACT 244

RESULT 7
US-09-524-168-2
Sequence 2, Application US/09524168
Patent No. 6452069
GENERAL INFORMATION:
APPLICANT: Baltz, Rachel Y.
APPLICANT: Bidney, Dennis L.
APPLICANT: Huffman, Gary A.
APPLICANT: Lu, Guihua
APPLICANT: Scelionge, Christopher J.
APPLICANT: Steinmetz, Andre A.
TITLE OF INVENTION: SP3 PROMOTER AND METHODS OF USE
FILE REFERENCE: 5718-74
CURRENT APPLICATION NUMBER: US/09/524.168
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1000
TYPE: DNA
ORGANISM: Helianthus annuus
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..
NAME/KEY: misc_feature
LOCATION: (825)..
OTHER INFORMATION: Transcription Start Site begins at base No. 6452069 825
NAME/KEY: CDS
LOCATION: (929)..
US-09-524-168-2

Query Match 3.8%; Score 37.8; DB 4; Length 1000;
Best Local Similarity 73.8%; Pred. No. 0.07; DB 4; Length 1000;
Matches 48; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 104 CTTTGCAGGAACACAGAAATGATGCGATGACAGAGACTGTATCTGTTGACA 163
DB 936 CATTCACAGGACAAACCAAAATGACAGAGTTGCGAGAAACCGTATTTGGTTGATA 995
QY 164 AATTA 168
DB 996 AATTA 1000

RESULT 8
US-09-134-001C-2422/c

TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-616-368A-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 1; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 411 TGAACAAGAGAAATGTTTGGCTGCAGAAAACCTGTACCCACAGAAAAGTATC 470
DB 339 TGGAGCTGCTGAGAAAGTTCAGATGTGGGATTCGTATATGCTGCGGAGAAATAT 398
QY 471 AGCCAATGGCAGCCCATACCATTAAGAGCTGCTCCATGCAAGCCAGAGGCTGTAA 530
DB 399 TGGAGCTGGAAGCCCTGGCAGAAAACCTGTTCCGATGTGCAAAAGTGTGGAGAGCTCT 458
QY 531 AAGCCCTTCCAACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504

RESULT 11

US-09-054-298-2
Sequence 2, Application US/09054298
Patent No. 6136953
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yel, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-054-298-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 3; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 411 TGAACAAGAGAAATGTTTGGCTGCAGAAAACCTGTACCCACAGAAAAGTATC 470
DB 339 TGGAGCTGCTGAGAAAGTTCAGATGTGGGATTCGTATATGCTGCGGAGAAATAT 398

DB 339 TGGAGCTGCTGAGAAAGTTCAGATGTGGGATTCGTATATGCTGCGGAGAAATAT 398
QY 471 AGCCAATGGCAGCCCATACCATTAAGAGCTGCTCCATGCAAGCCAGAGGCTGTAA 530
DB 399 TGGAGCTGGAAGCCCTGGCAGAAAACCTGTTCCGATGTGCAAAAGTGTGGAGAGCTCT 458
QY 531 AAGCCCTTCCAACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504

RESULT 12

US-08-818-655-2
Sequence 2, Application US/08818655
Patent No. 6258557
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yel, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-818-655-2

Query Match
Best Local Similarity 50.6%; Score 34.8; DB 4; Length 741;
Matches 84; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 411 TGAACAAGAGAAATGTTTGGCTGCAGAAAACCTGTACCCACAGAAAAGTATC 470
DB 339 TGGAGCTGCTGAGAAAGTTCAGATGTGGGATTCGTATATGCTGCGGAGAAATAT 398
QY 471 AGCCAATGGCAGCCCATACCATTAAGAGCTGCTCCATGCAAGCCAGAGGCTGTAA 530
DB 399 TGGAGCTGGAAGCCCTGGCAGAAAACCTGTTCCGATGTGCAAAAGTGTGGAGAGCTCT 458
QY 531 AAGCCCTTCCAACTATACCGCATGAGGGGCGCTTATATTGTAA 576
DB 459 TGAATCAACAACCTGACTGAAAAGAGTGAATCTATTGTAA 504

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RESULT 13
US-08-616-368A-7
; Sequence 7, Application US/08616368A
; Patent No. 5767262
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/616,368A
; FILING DATE: 15-MAR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/022001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 880 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-616-368A-7

Query Match          3.5%; Score 34.6; DB 1; Length 880;
Best Local Similarity 49.2%; Pred. No. 0.63;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 112 GGAACACACAGAAATGATGCGATGTGACAAAGCTGTCTATCTGTTGACAAATTAAT 171
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DB 394 GGAGGTGCTGAGAAAGTCTCCAGATGTGGGATTCGTGTATCTCTGTCGAGAAATCAAT 453

QY 172 GCAGATAACAGATCTATACAAAGCTTGTTCAGATGCCATACATGCAAGGCGACTGTC 231
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 454 GGAGCTGGAAGCCCTGGCACAATAACTGTTCGATGTGCCAAGTGTGGGAAGACTCTG 513

QY 232 AAGCTTGGCACTACATTCCTTTGAGGAGAGTCTCTACTGTAGACCAACTTTGATCAG 291
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 514 GAGTCTACAACCTGACTGAGAGGAAGGTGAATCTACTGTAAGGGTCTACGCAAG 573

QY 292 CTCCTT 296
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DB 574 AACTT 578
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RESULT 14
US-09-054-298-7
; Sequence 7, Application US/09054298
; Patent No. 6136953
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar

APPLICANT: Jain, Mukesh
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298
FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 55...633
US-09-054-298-7

Query Match          3.5%; Score 34.6; DB 3; Length 880;
Best Local Similarity 49.2%; Pred. No. 0.63;
Matches 91; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 112 GGAACACACAGAAATGATGCGATGTGACAAAGCTGTCTATCTGTTGACAAATTAAT 171
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 394 GGAGGTGCTGAGAAAGTCTCCAGATGTGGGATTCGTGTATCTCTGTCGAGAAATCAAT 453

QY 172 GCAGATAACAGATCTATACAAAGCTTGTTCAGATGCCATACATGCAAGGCGACTGTC 231
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 454 GGAGCTGGAAGCCCTGGCACAATAACTGTTCGATGTGCCAAGTGTGGGAAGACTCTG 513

QY 232 AAGCTTGGCACTACATTCCTTTGAGGAGAGTCTCTACTGTAGACCAACTTTGATCAG 291
    |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
DB 514 GAGTCTACAACCTGACTGAGAGGAAGGTGAATCTACTGTAAGGGTCTACGCAAG 573

QY 292 CTCCTT 296
    |||
DB 574 AACTT 578

RESULT 15
US-08-818-655-7
; Sequence 7, Application US/08818655
; Patent No. 625857
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-Eh
; APPLICANT: Haber, Edgar
; APPLICANT: Jain, Mukesh
; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
```

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NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 880 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 55...633
OTHER INFORMATION:
US-08-818-655-7

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[illegible]

Search completed: November 22, 2002, 23:36:53
Job time : 71 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 23:02:28 ; Search time 57 Seconds

(without alignments)
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Title: US-09-928-412-1

Sequence: 1 gaattcgccgcgcgttccaaa.....cttgagcgcgcgcgaattc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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2: /cgn2_6/ptodata/1/pubpna/PC7_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	988	100.0	988	US-09-928-412-1	Sequence 1, Appli
2	295.4	29.9	744	US-09-770-149-39	Sequence 39, Appli
3	197.4	20.0	418	US-09-878-574-30	Sequence 30, Appli
4	192.2	19.5	396	US-09-878-574-3019	Sequence 3019, Ap
5	141.6	14.3	693	US-09-770-149-291	Sequence 291, App
6	132.2	13.4	345	US-09-878-574-22	Sequence 22, Appli
7	108.2	11.0	391	US-09-878-574-458	Sequence 458, App
8	100.2	10.1	378	US-09-878-574-1429	Sequence 1429, Ap
9	96.4	9.8	373	US-09-878-574-964	Sequence 964, App
10	94.2	9.5	405	US-09-878-574-3948	Sequence 3948, Ap
11	89.6	9.1	264	US-09-878-574-14576	Sequence 14576, A
12	83.6	8.5	280	US-09-294-093B-3904	Sequence 3904, Ap
13	82	8.3	279	US-09-294-093B-4538	Sequence 4538, Ap
14	79.4	8.0	296	US-09-878-574-3381	Sequence 3381, Ap
15	78.2	7.9	1081	US-09-789-919-5	Sequence 5, Appli
16	78	7.9	2379	US-09-880-192-13	Sequence 13, Appli
17	78	7.9	3336	US-09-833-381-1727	Sequence 1727, Ap
18	74	7.5	330	US-09-294-093B-3580	Sequence 3580, Ap
19	73.2	7.4	397	US-09-789-919-41	Sequence 41, Appli

20	71.6	7.2	732	10	US-09-925-297-152	Sequence 152, App
21	71.6	7.2	2749	10	US-09-822-849A-399	Sequence 399, App
22	70.2	7.1	743	10	US-09-789-919-6	Sequence 6, Appli
23	66	6.7	276	10	US-09-878-574-13619	Sequence 13619, A
24	63.8	6.5	705	10	US-09-833-381-1735	Sequence 1735, Ap
25	63.8	6.5	1299	10	US-09-833-381-1733	Sequence 1733, Ap
26	63.4	6.4	521	10	US-09-833-381-1730	Sequence 1730, Ap
27	52.2	5.3	643	10	US-09-833-381-1736	Sequence 1736, Ap
28	46.4	4.7	355	10	US-09-770-791-626	Sequence 626, App
29	43.2	4.4	276	10	US-09-878-574-14665	Sequence 14665, A
30	41.8	4.2	2251	10	US-09-796-256A-11	Sequence 11, Appli
31	40.8	4.1	167	10	US-09-294-093B-3953	Sequence 3953, Ap
32	40.8	4.1	738	10	US-09-910-943-6	Sequence 6, Appli
33	40	4.0	1273	10	US-09-773-926-1	Sequence 1, Appli
34	40	4.0	1273	10	US-09-773-926-2	Sequence 2, Appli
35	40	4.0	1273	10	US-09-773-926-3	Sequence 3, Appli
36	37.4	3.8	288	10	US-09-923-876-5837	Sequence 4931, Ap
37	37.2	3.8	248	10	US-09-960-352-2919	Sequence 5837, Ap
38	36.8	3.7	413	10	US-09-960-352-2919	Sequence 2919, Ap
39	36.4	3.7	84539	10	US-09-962-436-36	Sequence 36, Appli
40	35.2	3.6	406	10	US-09-960-352-10265	Sequence 10265, A
41	35	3.5	1938	10	US-09-841-132-532	Sequence 532, App
42	34.8	3.5	237	10	US-09-960-352-14543	Sequence 14543, A
43	34.8	3.5	385	10	US-09-960-352-1739	Sequence 1739, Ap
44	34.8	3.5	1084	9	US-09-938-842A-3786	Sequence 3786, Ap
45	34.8	3.5	2000	10	US-09-887-576-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-928-412-1
Sequence 1, Application US/09928412
Patent No. US20020123623A1
GENERAL INFORMATION:
APPLICANT: KAWAKURA, Akiyoshi
APPLICANT: EBINUMA, Hiroyasu
TITLE OF INVENTION: TRANSCRIPTION FACTOR CONTROLLING PHENYLPROPANOID
FILE REFERENCE: 4859-0027-0
CURRENT APPLICATION NUMBER: US/09/928,412
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/282,146
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 10-125171
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 988
TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: CDS
LOCATION: (100)..(702)
NAME/KEY: misc.feature
LOCATION: (127)..(282)
OTHER INFORMATION: LIM domain
NAME/KEY: misc.feature
LOCATION: (427)..(582)
OTHER INFORMATION: LIM domain
US-09-928-412-1

Query Match 100.0% ; Score 988; DB 10; Length 988;

Best Local Similarity 100.0% ; Pred. No. 2.1e-260; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGCGCCGTTCCAAAACCAAGTGTACACAAAGGGAAGGACACCAAG 60
|||||
Db 1 GAATTCGCGCCGTTCCAAAACCAAGTGTACACAAAGGGAAGGACACCAAG 60
QY 61 ACCATTTTGTTCGTGTAACCTGCTGTATATAGCCATGCGTTTTCAGAGACCA 120


```
; Sequence 30, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 30
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-007-Q1-B1-D7
US-09-878-574-30
```

```
Query Match          20.0%; Score 197.4; DB 10; Length 418;
Best Local Similarity 79.4%; Pred. No. 1.4e-44;
Matches 247; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGACGAGACACAGAAATGATGATGATGACAGACTGTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 110 ATGGCATTTGACAGACACAGAGAGTATGCTGTGACAAACCGTTTATCTGTT 169

QY 160 GACAAATTAACGTGACATTAACAGATCTATCACAAGCTTTGTTGATGCCATCTG 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 170 GATAGTTTACCGGATACCGAGTTTTCACAAAGCTTGTCTGATGCTTATCTG 229

QY 220 AAGGCACATGTCAGCTTGCACATTCCTTGTGAGGAGCTTCTATCTGTAACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 230 AAGGACACCTTCAGCTGAGCAACTGCTTTTGAGGAGTCTTTATTTGTAAGCA 289

QY 280 CACTTGTACGCTTTCACAACAACTGCGAGTTTGGATTAAGCTTTGAAGTACCA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 290 CACTTGGACCAACTGTTCAAAAGAACAGGAGCTTGACAAAGCTTTGAAGAACCA 349

QY 340 AAAAATGTAGCCACAGAAACCCATTGACAGTACAGTACAGTACCAAGTACCA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 350 AAAATGTCAGCCAGAGAAATTTTGA--AGAGAACTGTGACAGCAAAAGTCTCA 406

QY 400 AGCATGTTTG 410
    ||||| |||||
DB 407 AGTATGTTTG 417
```

```
RESULT 4
US-09-878-574-3019
; Sequence 3019, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3019
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-017-Q1-B1-C11
US-09-878-574-3019
```

```
Query Match          19.5%; Score 192.2; DB 10; Length 396;
Best Local Similarity 78.6%; Pred. No. 3.7e-43;
Matches 243; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY 100 ATGGCTTTTGACAGACACACAGAAATGATGATGATGACAGACTGTATCTGTT 159
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 91 ATGGCATTTTGACAGAGAACCCGAAAGTATGCTGTGACAAACCGTTTATCTGTT 150

QY 160 GACAAATTAACGTGACATTAACAGATCTATCACAAGCTTTGTTGATGCCATCTG 219
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 151 GATAGTTTACCGCGGATTAACGAGTTCACAAAGCTTGTGAGATGCCATCTG 210

QY 220 AAGGCACGTGACAGCTTGCACATTCCTTGTGAGGAGTCTTATCTGTAACCA 279
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 211 AAGGAAACCTTCAGCTGACACTTAACTCTTTGTGAGGAGTCTTCTTACGCAAGCA 270

QY 280 CACTTGTACGCTTTCACAAACAACTGCGAGTTGGATTAAGCTTTGAGTACCA 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 271 CATTTGACCACTGTTCAAAAGACTGGAGCTTGACAAAAGCTTTGAGGACACCA 330

QY 340 AAAAATGTAGCCACAGAAACCCATTGACAGTACAGAGAACACAGGTTAGCAAGTGACA 399
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 331 AAATGTCAGCCAGCCAGAGAAATTTTGA--AGAGAACTGTGACAGCAAAAGTCTCA 387

QY 400 AGCATGTTT 408
    ||||| |||||
DB 388 AGTATGTTT 396
```

```
RESULT 5
US-09-770-149-291/c
; Sequence 291, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameeka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickert, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neill
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 291
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(693)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-291
```

```
Query Match          14.3%; Score 141.6; DB 10; Length 693;
```

Best Local Similarity 58.9%; Pred. No. 3,2e-28;
Matches 290; Conservative 0; Mismatches 184; Indels 18; Gaps 2;

```
QY 122 AGAATTCATGGCATGTGACACAGAGCTGTATCTGTGACAAATTAAGTCAGATAACA 181
    ||||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 687 ACAATTCATGGTGTGTATAGACAGCTATGTGTGTGACATGTGTGCTTGAAGAA 628
QY 182 GAATCTATCACAAGCTTTGTTTCAGATGCCATCTAGCAGAGGCACTGCAAGCTTGCA 241
    || ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db 627 TGCCCTTACACAGCTTGTCTTCAAGGTGTACCCATTTGCAAGAAACCTTCAGATGAGCA 568
QY 242 ACTACAATTCCTTTGAGGAGTCTTATATCTAGACCAACACTTTGATCAGCTCTTCAAC 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 567 ACTATTCTCTCATGTGATGAGTGTGTGTGATGACAGACTCATTTGAGCAACTCTTCAAG 508
QY 302 AAATGCGACGTTTGGATTAAGCTTTGAGGTAGACCAAAAATGTGAAGCCACAGAAAC 361
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 507 AATGTGCAATTTGACGAAAAAATTTTCA---CCAGGAAAAACGAGAGCCACAGCTGCA 451
QY 362 CCATTGACAGTGCAGAAACACAGGTAGCCAAAGTGCAGACAGCTTTGGTGAACAAGAG 421
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 450 CTA-----GGACTCCAGCAAGATATCTCTCTCTGTGTGGAACACAG 406
QY 422 AGAATGTTTTGGCTGCAAGAAACGTCTTACCAACAGAAAGTATCAGCCATGGCA 481
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 405 ACAAGTGTCCCGCTTGCAAAAAACGTCTTACCTTTGAAAGATACAAATGGAAGAG 346
QY 482 CGCCATACATTAAGAGCTGTTCCATGCAAGCCAGAGGCTGTATATAAGCCCTTCCA 541
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 345 AATGCTTCCACAAAGACATGTTGCGGTGCGCTACGGGTGGTGTACCTGACTACCTCT 286
QY 542 ACTATACCGCATGAGGCGGCTTATATTTGAACATCACCATATTTCACTATCAAG 601
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 CTTACGCGCTCTTATAGGCTTCTCTATTTGCCGACATCACTTAACCAACTTTCATGG 226
QY 602 AGAAGGCACT 613
    ||||| |||||
Db 225 AGAAGCAAACT 214
```

RESULT 6
US-09-878-574-22

```
; Sequence 22, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 22
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(345)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB9028-028-Q1-B1-F3
US-09-878-574-22
```

Query Match 13.4%; Score 132.2; DB 10; Length 345;
Best Local Similarity 78.6%; Pred. No. 8.5e-27;
Matches 158; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

```
QY 105 TTTTGAGAACACACAGAAATGCATGGATGTGACAGAGCTGTATCTGTGTTGACAA 164
    ||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 145 TTTTGAGAACACACAGAAATGCATGGCTTGTGCCAAAAGCTGTATCTTGTGATAA 204
QY 165 ATTAAGTCAGATTAACAGAAATCTATTCACAAAAGCTTTGTTGATGCCATCAGCAAGG 224
    ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 205 GTTAAGTCAGATTAAGCGGTGTCTATTCATTAAGGCTTGTGCGATGCCACCATTTGCCGTA 264
QY 225 CACTGTCAAGCTTGGCAACTAACAATTCCTTTGAGGAGAGTCTATATCTAGACCAACTT 284
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 265 TACCCTTAAGCTTGAAGCACTACTGTCTTTTGAAGGGGTGCTCTACTGACAGACTCACTA 324
QY 285 TGATCAGCTCTTCAACAAAC 305
    ||||||| ||||| ||||| |||||
Db 325 TGATCAACTCTACAGCAAGC 345
```

RESULT 7
US-09-878-574-458

```
; Sequence 458, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 458
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB9028-050-Q1-B1-G11
US-09-878-574-458
```

Query Match 11.0%; Score 108.2; DB 10; Length 391;
Best Local Similarity 65.6%; Pred. No. 3.3e-20;
Matches 158; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

```
QY 90 GATATATGCGATGCTTTTTCAGAGAACACACAGAAATGCATGGATGTGACAGAGCTGT 149
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GAAACAAACATGTCAATTCACAGAACTTGTATTAATGCACAGCATGTGCAAGACTGT 180
QY 150 CTATGCTGTGACAAATTAAGTGCAGATATACAGATCTATCACAAGCTTTGTTGAGATG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CTATGCTGTGACTTGTATCTTTGAAGAAATTCCTTACCATTAATAAACTGCTTCAAGTG 240
QY 210 CCATCACTGCAAGGACACTGTCAAGCTTGCACATCAATTCCTTTGAGGAGTTCATATA 269
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CACTCACTGCAAGGAGTGTCTTACGATGTGACATCTCTCATATGATGATTTCTTTA 300
QY 270 CTGTAGCACACACTTGTATCAGCTCTTCAACAACACTGCGAGTTTGGATTAAGACTTTGA 329
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TTGCAAGACACATTTGAACAGCTTTCAAGGAATCTGGCAATTTGACAAAGAACTTCCG 360
QY 330 A 330
Db 361 A 361
```

RESULT 8
US-09-878-574-1429

```
; Sequence 1429, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
```



```
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1429
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-037-Q1-B1-G7
US-09-878-574-1429
```

```
Query Match          10.1%; Score 100.2; DB 10; Length 378;
Best Local Similarity 66.4%; Pred. No. 4.9e-18;
Matches 144; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
```

```
QY 98 CCATGCGTTTGCAGACACACACAGAAATGCATGCGATGACAGACTGCTATCTGG 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 151 CAATGTCATTGACAGAGAACTACAGTAAATGCAAGGCTTGATTAAGACTGTTATGTGG 210
QY 158 TTGACAAATTAATCTGCAGATTAACAGATCTATGACAAAGCTTTGTCAGATGCATCACT 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 ATGACATGTAATCTTTGAAGGATATACCTTACCATAGAACTGCTTACATGACAGTCACT 270
QY 218 GCAAGGGCACTGTCAAGCTTGGCACTACAATTCTTTGAGGAGTTCTTACTGTAGAC 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 271 GCAAGGAGATACGACAGATGATACCTACGCCACAGATGATGATGCTCTCTATTTGCAAGC 330
QY 278 CACACTTTGATCAGCTCTTCAACAAACTGGCAGTTT 314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 CACACTTTGAAACGCTTTTCAAGAACTGTGCAATTT 367
```

```
RESULT 9
US-09-878-574-964
```

```
; Sequence 964, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 964
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1):(373)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-044-Q1-B1-B10
US-09-878-574-964
```

```
Query Match          9.8%; Score 96.4; DB 10; Length 373;
Best Local Similarity 66.2%; Pred. No. 5.3e-17;
Matches 139; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
```

```
QY 100 ATGCGTTTTCAGAGACACACAGAAATGCATGCGATGACAGACTGCTATCTGTT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 ATGCGATTTCAGCGGAGCCCAAGAAATGCAAGCTTGCACAAACTGTTCACTTGCTC 174
QY 160 GACAAATTAATCTGCAGATTAACAGATCTATCACAAGCTTTGTTCAATGCATCACTGC 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 GAAGGTTTATCTGTCATGGGGCTGCTTATCACAAGAAATTTCTTCAATGACGACCTTGC 234
```

```
QY 220 AAGGCACTGTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGTTCATATCTGTAGACCA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AATGGCCTTCTGCGAATTAACCACTACTCATCCAGGAGGGTTTGTACTGCAAGGTG 294
QY 280 CACTTTATCAGCTCTTCAACCAACTGGC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 CACTTTGAGCAGCTTTTCAAGAAACTGGC 324
```

```
RESULT 10
US-09-878-574-3948
```

```
; Sequence 3948, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3948
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-003-Q1-B1-E7
US-09-878-574-3948
```

```
Query Match          9.5%; Score 94.2; DB 10; Length 405;
Best Local Similarity 65.4%; Pred. No. 2.2e-16;
Matches 138; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
```

```
QY 100 ATGCGTTTTCAGAGACACACAGAAATGCATGCGATGACAGACTGCTATCTGTT 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 115 ATGCGATTTCAGCGGAGCCCAAGAAATGCAAGCTTGCACAAACTGTTCACTTGCTC 174
QY 160 GACAAATTAATCTGCAGATTAACAGATCTATCACAAGCTTTGTTCAATGCATCACTGC 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 GAAGGTTTATCTGCGAATTAACCACTACTCATCCAGGAGGGTTTGTACTGCAAGGTG 234
QY 220 AAGGCACTGTCAAGCTTGGCAACTACAAATTCCTTTGAGGAGTTCATATCTGTAGACCA 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 AATGGCCTTCTGCGAATTAACCACTACTCATCCAGGAGGGTTTGTACTGCAAGGTG 294
QY 280 CACTTTGATCAGCTCTTCAACCAACTGGCA 310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 CACTTTGAGCAGCTTTTCAAGAAACTGGAA 325
```

```
RESULT 11
US-09-878-574-14576
```

```
; Sequence 14576, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 14576
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Glycine max
```

Query Match	8.08;	Score 79.4;	DB 10;	Length 296;
Best Local Similarity	66.9%;	Pred. No. 2.1e-12;		
Matches 113;	Conservative 0;	Mismatches 56;	Indels 0;	Gaps 0;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2002, 22:12:03 ; Search time 1964 Seconds

(without alignments)
8147.220 Million cell updates/sec

Title: US-09-928-412-1

Perfect score: 988
Sequence: 1 gaattcgcgccgttccaaa.....cttgagcgcgccgaattc 988

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estrov:*
6: em_estcpl:*
7: em_estcro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381.2	38.6	537	14	BQ115637 EST601213
2	361.8	36.6	755	9	AJ498553 AJ498553
3	361.6	36.6	714	14	BU014288 BU014288
4	361.6	36.6	740	14	BU008321 BU008321
5	360.2	36.5	645	14	BQ148732 BQ148732
6	360	36.4	690	14	BO857598 BO857598

7	358.6	36.3	782	10	AM559538
8	344.4	34.9	698	10	BE203860
9	333.2	33.7	538	13	B1129342
10	330.4	33.4	593	12	BC043927
11	326.8	33.1	548	10	BE440655
12	313.2	31.7	589	14	BO741219
13	312.4	31.6	656	14	BO623451
14	310.2	31.4	657	12	BF638624
15	309.6	31.3	535	13	BM178858
16	309	31.3	581	12	BF425662
17	302.6	30.6	553	10	BE210592
18	300.8	30.4	503	12	BC362712
19	298.8	30.2	548	10	AW761298
20	298.4	30.2	531	10	AM559283
21	297.8	30.1	571	10	BE473593
22	295.6	29.9	527	14	BO785792
23	295	29.9	580	10	AV831505
24	294.4	29.8	631	14	BO629770
25	292.4	29.6	647	12	BG138218
26	289.2	29.3	514	9	A1930682
27	287	29.0	471	13	BM173395
28	286	28.9	693	13	BM301553
29	282.6	28.6	950	11	AY112454
30	282.2	28.6	624	14	BO048239
31	282	28.5	641	14	BQ134245
32	281	28.4	585	12	BG156003
33	280.2	28.4	543	14	BO514084
34	279	28.2	506	13	BM143254
35	275.6	27.9	561	13	BM178019
36	271	27.4	647	14	BQ279385
37	271	27.4	670	13	BM299814
38	270.2	27.3	599	14	BU037830
39	268.6	27.2	536	13	B1417129
40	268.6	27.2	536	13	B1674161
41	268.6	27.2	667	12	BC454148
42	268.2	27.1	846	14	BO752856
43	267.8	27.1	559	12	BF146081
44	266.6	27.0	655	10	BE443538
45	266.4	27.0	632	12	BG140591

ALIGNMENTS

RESULT 1
LOCUS BQ115637 537 bp mRNA linear EST 22-JUL-2002
DEFINITION EST601213 mixed potato tissues Solanum tuberosum cDNA clone STMDCS1
5' end, mRNA sequence.

ACCESSION BQ115637
VERSION BQ115637.2 GI:21917057
KEYWORDS EST

SOURCE potato.

ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 537)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., Van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.

AUTHORS
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Apr 17, 2002 this sequence version replaced gi:20167599.

CONTACT: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatoc@tigr.org

FEATURES
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cdna@resgen.com
Seq primer: T3.
Location/Qualifiers

Query Match	Best Local Similarity	84.4%	Pred. No. 1.3e-83	Matches 444	Conservative 0	Mismatches 73	Indels 9	Gaps 1
QY 98	CCATGGCTTTTCGAGGACACACAGAAATGCATGGCATGTCTATCTGG 157							
Db 21	CAATGGCTTTTCGAGGACACACAAATATGTATGCGATGAAAAAGACAGTATTTGG 80							
QY 158	TTGACAAATTAACCTGCAGATTAACAGATCTATACCAACCTGTTCAATGCCATCACT 217							
Db 81	TTGATTAATTAACCTGCAGACAAATAGAGTCTTCTATTAATACTGTTTAAATCCATCACT 140							
QY 218	GCAGGGCACTGTCAAGCTTGGCACTACATATCTGTTAGGAGAGTTCTATCTGTAGAC 277							
Db 141	GCAGGGCACTGTCAAGCTTGGCACTACATATCTGTTAGGAGAGTTCTATCTGTAGAC 200							
QY 278	CACACTTTGATACGCTCTTCAACAACACTGGCAGTTTGGATAAAAGCTTTGAAGGTACAC 337							
Db 201	CCCACTTTGATACGCTCTTCAAAAAGACTGGAAGCTTGTACAAAAGCTTTGAAGGGACAC 260							
QY 338	CAAAAATGTGAAGCCACAGAAACCCATTGACAGTGAAGAAACACAGATGACCAAAAGTGA 397							
Db 261	CAAAAATGTGAAGCCACAGGAAA-----GATGAGAAACCCACAGGAGCTTAAGTTT 311							
QY 398	CAAGCATGTTTGTGGAGACAAAGAGAAATGTTTGGCTGCAAGAAACTGTCTACCCAA 457							
Db 312	CAAGCATGTTTGTGGAGACAAAGAGAAATGTTTGGCTGCAAGAAATGTTTATCCAA 371							
QY 458	CAGAAAGATATCAGCCAAATGGCAGCCATACCATTAAGAGCTGCTTCCATCCAGCAGCAG 517							
Db 372	CAGAAAGATATCTGTGATGGAAACACCATACCAAAAAGTTGCTTCAATGTAGCCAGT 431							
QY 518	GAGGCTGTCTAATAAGCCCTTCCAACTATACCGCACATGAGGGGGCTTATATTGTAAC 577							
Db 432	GAGGCTGTCTAATAAGCCCTTCCAACTATATTGCTACAGAAAGGGCGCTCTACTGCAAGC 491							
QY 578	ATCACCATATTCACCTATTCAGAGGAAAGGGCACTTAAGCAAGCT 623							
Db 492	ATCACCATGTTCACTGATCAAGGAAAGAAAGAACTTATGACCAACT 537							

source 1. 537

/organism="Solanum tuberosum"

/cultivar="Kennebec or Blinje"

/db_xref="taxon:4113"

/clone="STMDC51"

/clone.lib="mixed potato tissues"

/tissue.type="mixed tissues"

/lab.host="SOLR"

/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; Supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes 'tubers, or roots.'"

BASE COUNT	187 a	103 c	113 g	134 t
ORIGIN				

Query Match 38.6%; Score 381.2; DB 14; Length 537;

Best Local Similarity 84.4%; Pred. No. 1.3e-83;

Matches 444; Conservative 0; Mismatches 73; Indels 9; Gaps 1;

RESULT 2

LOCUS AJ498553 755 bp mRNA linear EST 09-AUG-2002

DEFINITION AJ498553 MTPOSE Medicago truncatula cDNA clone mt--acc955206a09, mRNA sequence.

ACCESSION AJ498553

VERSION AJ498553.1 GI:22088996

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 755)

Finthaber,C., Bartelsmeyer,V., Meyer,F., Bartels,D., Bekel,T.,

AUTHORS

TITLE Linke,B., Puehler,A. and Kuester,H.
 Determination of transcript sequences from developing pods
 JOURNAL Unpublished seeds of Medicago truncatula genotype A17
 COMMENT Unpublished (2002)
 Contact: Kuester H
 Lehrstuhl fuer Genetik
 Universitaet Bielefeld
 Postfach 100131, D-33501 Bielefeld, Germany.
 FEATURES
 source
 1. 755
 Location/Qualifiers
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="mc-acc935206a09"
 /clone_lib="MTPPOSE"
 /tissue_type="pods including seeds"
 /dev_stage="different stages of development"
 /note="Vector: pGEM-T, Site.1: PstI; Site.2: SphI;
 genotype A17; cDNA was prepared from polyA+ enriched RNA
 from developing pods including seeds harvested at
 different stages of development. The cDNA was
 directionally ligated by Medigenomix into the pGEM-T
 vector from Promega using GCATGCGCGCCGCGCCGACATG and
 CTCGAGGCCATTATGCGCCGGC adaptors. Plasmids containing cDNA
 inserts were propagated in E. coli DH10B cells."
 BASE COUNT 252 a 136 c 150 g 217 t
 ORIGIN
 Query Match 36.6%; Score 361.8; DB 9; Length 755;
 Best Local Similarity 77.5%; Pred. No. 8; 4e-79;
 Matches 438; Conservative 0; Mismatches 127; Indels 0; Gaps 0

OY	100	ATGGCTTTTGGCAGGAACCCACGAAGAATGCATGGGATGTGACAAAGCCTGTCTATGGT	159
OY	113	ATGGCATTTTGGCAGGAACCACTCAGAAAGTGTATGGCTTGTACAAAACAGTTATCTTGT	172
OY	160	GACAAATTAACTGCAGATTAACAGAAATCTATATCCAAAGCTTGTTCAGATGCCATCAGC	219
Db	173	GATAGTTAACTGCTGATATAGAAATTTTCCACAAAGCTTGTTTCAGATGTCACCACTGC	232
OY	220	AAGGCACCTGTCAACCTTGGCAGATCAATCCCTTTGAGGGAGTCTATAGCTAGACCA	279
Db	233	AAGGAAACCCCTAACCTTAAGCAACACTACATATCTTTTGGAGGAGTCTTACTGCAGACCA	292
OY	280	CACCTTTGATCAGCTCTTCAAAACAACTGGCAGTTTGGATAAAAGCTTTGAAAGTACACCA	339
Db	293	CACCTTGCACCACTGTCCAAAAGAACTGGTACCTTTGAGAAAAGCTTTGAAAGGACACGG	352
OY	340	AAAAATGTGAAGCCACAGAAACCCATTGCACTGTGAGAAAACCAACAGTACGCCAAATGACA	399
Db	353	AAAAATGTCAAGCCAGAAAAGAAATTAAGATTAATGAAAACCTGTGCAGACTTAAACCTTCA	412
OY	400	AGCATGTTTGGTGGAGAACAGAGAGAAATGTTTGGCTGCAGAAAACGTGTACCCACACA	459
Db	413	AGTATGTTTGGTGGAGAACAAAGSAGCAAAATGTTCTGGTTTGCAGAAAACAGTATCCACT	472
OY	460	GAAAGGTATCAGCCAAATGCCACGCCATTAACCTTAAGAGCTGCTTCCAATGCAAGCCAGGA	519
Db	473	GAGAAAGTTTACAGTAAATGAACCTCTTAACCACTTAAGAGTGTGTTCAAAATGTTGTATGGA	532
OY	520	GGCCTGTAAATTAAGGCCCTTCCAACTATTAACCCAGCATGAGGGGCGCTTTATTTGTTAAACT	579
Db	533	GGGTCTACTATCAGTCCCTTCCAAATTACATAGCAGCATGAGGAGAAAATTTCTACTGCAAAACG	592
OY	580	CACCATATTCAACTTATCAAGAGAGAGGSCAACTTAAAGCAACCTTGTAGGGTGACATGAA	639
Db	593	CACCATATTCAACTGATCATCAAGCAAAAAGAAATTTAAAGCCAGTGAAGAGTGACCATAG	652
OY	640	ATGATTTCCAGACAAACAAGAG 664	
Db	653	AAAAATGCTGGGAAAATCAATGCTG 677	

LOCUS	B0U14288		714 bp	mRNA	linear	EST 22-AUG-2002
DEFINITION	B0U14288	OQ6P601.yg.ab1	OQ_EFGHU lettuce serritola	Lactuca sativa	CDNA clone	
ACCESSION	B0U14288	OQ6P601	mRNA sequence.			
VERSION	B0U14288.1	GI:22448683				
KEYWORDS	EST.					
SOURCE	Lactuca sativa.					
ORGANISM	Lactuca sativa					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;					
AUTHORS	Lactuca.					
TITLE	1 (bases 1 to 714)					
JOURNAL	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Liu,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison ,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project http://compenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmudson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig OQ_CA_contig6843, see http://cgpdb.ucdavis.edu/ for details. Plate: OQ66 row: P column: 01.					
COMMENT	Location/Qualifiers					
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	/clone="OQ6P601"					
	/clone_id="OQ_EFGHU lettuce serritola"					
	/lab_host="E.coli"					
	/note="Vector: pBRCSNFIAB. The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/ TAG_LIB=OQ_EFGHU lettuce serritola TAG_TISSUE=flowers pre-fertilized TAG_SEQ=CGTTGACGGC"					
BASE COUNT	209 a	161 c	151 g	193 t		
ORIGIN						
Query Match	36.6%	Score 361.6;	DB 14;	Length 714;		
Best Local Similarity	81.0%;	Pred. No. 9.3e-79;				
Matches 421;	Conservative 0;	Mismatches 99;	Indels 0;	Gaps 0;		
OY	115	ACCACACAGAATGATGCATGTGACAAAGACTGCTATCTGTGGTGAACAATAA	TAAC	TCA	174	
Db	1	ACAACCCAGAAAATGATGGCATGTGACAAAGACTGTACTCTGGTGACAAAGCTCACTCA	60			
OY	175	GATACACAAATCTATCACAAAGCTGTTTCAGATGCCATCACTGCAGAGGCAC	TGTCA	NAG	234	
Db	61	GATTAATGCAATCTTCACAAAGCTTGCTTCAGATGCCACCATTTGCAAAAGGCA	CCTCA	NAG	120	
OY	235	CTTGCACTACAAATCTCTTGAGGAGCTTCTATCTAGTACACCACTTGTATCAG	CTC	294		
Db	121	CTTACCACTACAACTCTTGAGGAGCTTCTGATTGACAGGCACACTTGTATCA	CTC	180		
OY	295	TTCAACAACAACCTGCAGTTTGATTAAGCTTTGAAGTACACCAAATAATGTGA	GCCA	354		
Db	181	TTCAAGAAGACGTGTAGCTTGTAGCAAAAGCTTTGAAGCACACCAATTTTGA	GCCA	240		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
3355	Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lal, Z., Church, S., Jackson, L. and Birdford, K.	1 (bases 1 to 740)	Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmudson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu] belongs to contig Q6_Ca_contig196843, see http://cgpdb.ucdavis.edu/ for details.	
415	ACAAGAGAGAAATGTTTGGCTGCAAGAAACCTGTCTACCCACAGAAAGATATCAAGCC	474		
301	ACGACAGTAAATGTTTGGCTGCTGCAAAACACCGCTATCCACGTGAAAGGTTTCACTA	360		
475	AATGGCAGCCATATCAATTAAGAGCTGCTTCCATATGACGACGAGGCTGTATTAATAGC	534		
361	AATGGAATCTATACCAACAAAGGCTGTTCAAAATGATCTATGAGGATGTGTATCAGC	420		
535	CCCTTCACATATACCGCACAATGAGGGGGCTTATATTTGTAACATCACCATATTCACATT	594		
421	CCATTAACCTATATTTGCAATGAAAGTGCTCTACTATCTGACACACACACCCCACTC	480		
595	ATCAAGAGAGAGGCACTTAAGCAAGCTTGAAGGTGACG	634		
481	ATCAAGAGAGAGGTAACCTGAGCCAGCTGCAAGGTGACG	520		
RESULT 4				
LOCUS	BU008321	740 bp	mRNA	linear
DEFINITION	OGH7D23.yg ab1 OG_EFGH lettuce serriola			EST 22-Aug-2002
ACCESSION	OGH7D23, mRNA sequence.			
VERSION	BU008321			
KEYWORDS	BU008321.1 GI:22442716			
SOURCE	EST.			
ORGANISM	Lactuca sativa.			
	Lactuca sativa.			
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;			
	Lactuca.			
	1 (bases 1 to 740)			
	Kozik A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,			
	Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison			
	, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lal, Z.,			
	Church, S., Jackson, L. and Birdford, K.			
	Lettuce and Sunflower ESTs from the Compositae Genome Project			
	http://compenomics.ucdavis.edu/			
	unpublished (2002)			
	Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmudson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu] belongs to contig Q6_Ca_contig196843, see http://cgpdb.ucdavis.edu/ for details.			
	Plate: OGH7	row: D	column: 23.	
	Location/Qualifiers			
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	/clone="OGH7D23"			
	/clone_lib="OG_EFGH lettuce serriola"			
	/lab_host="E.coli"			
	/note="Vector: pRCNASTAB: The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/ TAG_LIB-OG_EFGH lettuce serriola TAG_TISSUE-flowers pre-fertilized			


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source
1..782
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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIR-19N4"
/clone_1bp="DSIR"
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medicaginis"
/dev_stage="roots harvested at 10 days post inoculation
with Phytophthora medicaginis"
/lab_host="E. coli strain XLOLR"
/note="Vector: pluescript SK-, Site_1: EcoRI, Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the uni-zap XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts.
Plasmids containing cDNA inserts were excised from the
recombinant lambda-zap phage using Ex-Assist helper phage

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RESULT 9
LOCUS      B1129342                538 bp    mRNA    linear    EST 31-DEC-2001
DEFINITION G089P41Y Populus cambium cDNA library Populus tremula x Populus
            tremuloides cDNA, mRNA sequence.
ACCESSION  B1129342
VERSION    B1129342.1
KEYWORDS   GI:18013313
SOURCE     Populus tremula x Populus tremuloides.
ORGANISM   Populus tremula x Populus tremuloides.
REFERENCE  1 (bases 1 to 538)
AUTHORS   Herzig, M., Aspberg, H., Erlandsson, R., Bjorkbacka, H., Hiltunen,
            T., Karlsson, J., Teerli, T., Gustafsson, P., Behlert, R., Jansson, S.,
            Nilsson, O., Sundberg, B., Nilsson, P., Uhlen, M., Sandberg, G. and
            Lundberg, U.
TITLE      Gene expression in Populus
JOURNAL    Unpublished (2001)
COMMENT    Contact: Erlandsson R
            Department of Biotechnology
            Royal Institute of Technology
            Teknikringen 30, Stockholm S-10044, Sweden
            Tel: 46 8 790 8287
            Fax: 46 8 245452
            Email: rikert@biochem.kth.se.
FEATURES   Location/Qualifiers
            source          1..538
                        /organism="Populus tremula x Populus tremuloides"
                        /db_xref="taxon:47664"
                        /clone_lib="Populus cambium cDNA library"
                        /note="Organ: cambium"
BASE COUNT      170 a      123 c      114 g      131 t
ORIGIN
Query Match      33.7%; Score 333.2; DB 13; Length 538;
Best Local Similarity 79.3%; Pred. No. 9.3e-72;
Matches 395; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 99 CATTGGCTTTGCGAGAACCCACACAGAAATGATGGCATGTGACAGACTGTATCTGCT 158
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DB 41 CATTGGCTTTGCGAGAACCCACACAGAAATGATGGCATGTGACAGACTGTATCTGCT 100
QY 159 TGAACAATTACGACGATGACAGAAATCTATCAAAAGCTGTTTCAGATGCCATCTG 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 101 GACACAGTTTACGACGATGATACCGTGTGTACACAGAGCTTGCTCGATGCCATCTAT 160
QY 219 CAAGGACACTGTCAAGCTTGGCACTACATTCCTTTGAGGAGTTCATATCTATAGACC 278
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 161 CAGAGAACCTTCAAGCTTGGCACTACATTCCTTTGAGGAGTTCATATCTATAGACC 220
QY 279 ACATCTTGTACACTCTTCAACAACAACTGGCAGTTGGATATAAGCTTTGAAGTACACC 338
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DB 221 ACATCTTGTACACTCTTCAACAACAACTGGCAGTTGGATATAAGCTTTGAAGTACACC 280
QY 339 AAAAATGTGAACACACAGAACCCATTCATGACAGTGAAGAACCAAGTACCAAGTAC 398
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 281 AAAAATGTGAACACACAGAACCCATTCATGACAGTGAAGAACCAAGTACCAAGTAC 340
QY 399 AAGCATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAATGCTTACCCAC 458
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 341 GACCATGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAATGCTTACCCAC 400
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      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 401 TGGAGAGGTTTGTGGAACAGAGAAATGTTTGGCTGCAAGAAATGCTTACCCAC 460
QY 519 AGGCTGTGTAATAGCCCTTCAACTATACGACATGAGGGGCGCTATATGTATAACA 578
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DB 461 AGCATGTACATTAAGCCATCACTACATTCATGACATGAAGGTGCTCTACTGCAACA 520

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QY 579 TCACCATATTCACACTAT 596
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DB 521 CCACACACACCAACTAT 538
RESULT 10
LOCUS      BG043927                593 bp    mRNA    linear    EST 28-NOV-2001
DEFINITION sa34h07.y1 Gm-cl059 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-cl059-1118 5', similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN
            LIM1.1, mRNA sequence.
ACCESSION  BG043927
VERSION    BG043927.1
KEYWORDS   GI:12490407
SOURCE     soybean.
ORGANISM   Glycine max
REFERENCE  1 (bases 1 to 593)
AUTHORS   Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khana,
            A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
            Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
            Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
            R., Riltter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
            R., Waterston, R. and Wilson, R.
TITLE      Public Soybean EST Project
JOURNAL    Unpublished (1999)
COMMENT    Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.edu
            This clone is available through: Resgen, Invitrogen Corp. 2130
            South Memorial Parkway Huntville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            High quality sequence stop: 418.
FEATURES   Location/Qualifiers
            source          1..593
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                        /issue_type="Whole seedling, 2 week old, etiolated"
                        /lab_host="DH10B"
                        /note="Vector: Bluescript II SK+; Site-1: EcoRI; Site-2:
                        XhoI; The cDNA library was constructed from mRNA isolated
                        from 2 week old etiolated whole seedlings of P1468916.
                        Complementary DNA was synthesized from mRNA using a primer
                        consisting of a poly(dt) sequence with a XhoI restriction
                        site. EcoRI adapters were ligated to the blunt-ended cDNA
                        fragments followed by XhoI digestion. The cDNA fragments
                        were directionally cloned into the EcoRI- XhoI restriction
                        site of the Bluescript vector. The ligated cDNA fragments
                        were transformed into DH10B host cells (Gibco BRL). This
                        library was constructed in the laboratory of Dr. Randy
                        Shoemaker at Iowa state university."
BASE COUNT      205 a      122 c      136 g      130 t
ORIGIN
Query Match      33.4%; Score 330.4; DB 12; Length 593;
Best Local Similarity 76.5%; Pred. No. 4.7e-71;
Matches 419; Conservative 0; Mismatches 126; Indels 3; Gaps 1;
QY 100 ATGCGCTTTTGCAGAACACACAAATGATGATGACAGATGCTATCTGCTT 159
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 21 ATGCGATTTTGCAGAACACACAAATGATGATGATGATGATGATGATGATGATGATG 80
QY 160 GACAAATTAACAGATGAACAGAAATCTATCAACAAGCTTGTTCAGATGCCATCTG 219

```

Db 81 GATAGTTGACCCGAGATAACCGAGTACCATTAAGCGTTCCTTCAGATGCACCACTGC 140
QY 220 AAGGCGCTGTCAGCTGGCACTACATTCCTTTAGGAGATCTTACTGTAGACCA 279
Db 141 AAGGAACACTCAAGCTCAGCACTATTAATCTTTGAAGAGATCTTACTGTAGACCA 200
QY 280 CACTTTGATCAGCTCTTCAAAACAACCTGGCAGTTTGTATTAACCTTTGAAGTACACA 339
Db 201 CACTTTGACCAACTGTTCAAAAAGAGATGTCTTGAACAAAGCTTGAAGGACACCA 260
QY 340 AAAATGTGAAGCCACAGAAACCATTTGACAGTACAGACAGGTAAGCAAGTACA 399
Db 261 AAAATTTCTTAACCAAGAAAACCGGGA--AGAGAAACCTGCAGCAACCAAGTCTCA 317
QY 400 AGCATTTGTTGGTGGACAGAAAGAGAAATGTTTGGCTGCAGAAACGTCCTACCAACA 459
Db 318 AGTATGTTTGGTGGTGAAGTACAGATTAATGTGGGCTTGTCAAGAAAGTGTATCCACT 377
QY 460 GAAAGGTATCAGCAATGGCAGCCATACCATTAAGAGCTGCTTCAATGCAGCCACGCA 519
Db 378 GAAAGGTATCAGCCGTAATGGAACCTCTTATCAAGAGTGTCTTCAATGCAGCATGCA 437
QY 520 GCGTGTATTAAGCCCTTCCACTATACGACATAGAGGCGCTTATATTTAAACAT 579
Db 438 GGGTGTATTAATGATCCCTCCACTACATGACACAGCAACCACTGACGACAC 497
QY 580 CACCATTTCACTTATCAAGGAGGAGGCACTTAAGCAAGCTTGAGGAGGACATGAA 639
Db 498 CACCATTTCACTGATCAAGAGAGAGGCAATTTAAGCAATTTGAAGGTGACCATGAG 557
QY 640 ATGAAATTC 647
Db 558 AAGAGTAC 565

RESULT 11
BE440655 548 bp mRNA linear EST 04-DEC-2001
LOCUS sr50603.y1 Gm-cl043 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl043-1662 5' similar to TR:Q9ZTN6 Q9ZTN6 PGP9B. ;, mRNA
sequence.
ACCESSION BE440655.1 GI:9440145
VERSION BE440655
KEYWORDS soybean.
SOURCE EST.
ORGANISM glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 548)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna
A., Bolla, B., Matra, M., Hillier, L., Kucaba, J., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Rifter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: curesgen.com
Insert length: 703 Std Error: 0.00
High quality sequence stop: 478.
Location/Qualifiers

source
1. 548
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-cl043"
/issue="Hypocotyl and Plumule, germinating seeds"
/lab="host=DH108"
/note="Vector: p773Pac (pharmacia); Site 1: EcoRI;
Site 2: NotI. This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the p773-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker."

BASE COUNT 186 a 114 c 123 g 124 t 1 others
ORIGIN

Query Match 33.1%; Score 326.8; DB 10; Length 548;
Best Local Similarity 76.6%; Pred. No. 3.6e-70;
Matches 413; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 100 ATGCTTTTGCAGAACCAACAGAAATGATGATGACAGACTGTCTATCTGTT 159
Db 12 ATGCGATTTTCAGAGAAACCTCAAGAGTGCATGCTTGTACAAACAGTTTATCGTGT 71
QY 160 GACAAATTAACAGATGATACAGAAATCTATCACAAAGCTGTTTACATGCCATCACTGC 219
Db 72 GATAGTTGACAGAGTAACCGAGTGTACATTAAGCTGTCTGATGATGCCACCACTGC 131
QY 220 AAGGCACTGTCAAGCTTGGCACTACATTCCTTTGAGGAGTCTTACTGTAGACCA 279
Db 132 AAGGAACACTCAAGCTTACCACTATTAACCTTTTGGAGGCGTCTTACTGACAGGCA 191
QY 280 CACTTTGATCAGCTCTTCAAAACAACCTGGCAGTTTGTATTAACCTTTGAAGTACACCA 339
Db 192 CACTTGCACCAAGCTGTCAAAAAGATGATGCTTGTACAAAAGCTTGAAGGACACCA 251
QY 340 AAAATGTGAAGCCACAGAAACCATTAAGAGAGAGAAACAGAGTACCAAGTACCA 399
Db 252 AAAATTTCTTAACCAAGAAAACCGGGA--AGAGAAACCTGCAGCAACCAAGTCTCA 308
QY 400 AGCATTTTGGTGGACAGAGAGAAATGTTTGGCTGCAAGAAACCTGTACCCACACA 459
Db 309 AGTATGTTTGGTGGAACTAGAGATAATGTGCCGCTGTCAAAAACAGGTATCCCACT 368
QY 460 GAAAGGTATCAGCAATGGCAGCCATACCATTAAGAGCTGCTTCAATGCAGCCACGCA 519
Db 369 GAAAGGTATCAGCTGTAAGTAACCTCTTATCACAGAGTGTTCATTAATCACTACCTGCA 428
QY 520 GCGTGTATTAAGCCCTTCCACTATACCGCAATAGAGGCGCTTATTTGAACAT 579
Db 429 GGGTGTATTAATGATCCCTCCACTACATTTGCACAGCAAGCAACCACTTACGAGACAC 488
QY 580 CACCATTTCACTTATCAAGAGAGGCACTTAAGCAAGCTTGAAGGCTGACCATGA 638
Db 489 CACCACTTCACTGATCAAGAGAGGTAATTTAAGCCCACTTGAAGGCTGACCATGA 547

RESULT 12
B0741219 589 bp mRNA linear EST 17-JUL-2002
LOCUS seq15909.y1 Gm-cl045 glycine max cDNA clone SOYBEAN CLONE ID: 5'
DEFINITION similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN WLIM1. ;, mRNA
sequence.
ACCESSION B0741219
VERSION B0741219.1 GI:21888006
KEYWORDS EST.

SOURCE	ORGANISM
soybean.	glycine max
Eukaryota:	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes:	Magnoliophyta; eudicotyledons; core eudicots;
Rosidae:	eurosid 1; Fabales; Fabaceae; papilionoideae; Phaseoleae;
Glycine.	
1 (bases 1 to 589)	
Shoemaker,R., Keim,P., Vodka,L., Erpelidg,J., Corvelli,V., Khana	
A., Bolla,B., Marra,M., Hillier,L., Kucab,T., Martin,J., Beck,C.,	
Wyle,T., Underwood,K., Stepien,M., Thibaut,B., Allen,M., Bowers	
,Y., Peterson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk	
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann	
,R., Waterston,R. and Wilson,R.	
Public Soybean EST Project	
Unpublished (1999)	
Contact: Shoemaker R/Public Soybean EST Project	
Public soybean EST Project	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: est@watson.wustl.edu	
This clone is available through: ResGen, Invitrogen Corp, 2130	
South Memorial Parkway Huntsville, AL 35801 For further information	
call: (800) -933-4363 or contact: ccu@resgen.com web site:	
www.resgen.com	
Seq primer: -40RP from Gldco	
High quality sequence stop: 431.	
FEATURES	
Source	
1..589	
/organism="Glycine max"	
/db_xref="taxon:3847"	
/clone="SOYBEAN CLONE ID:"	
/clone_lib="Gm-cl045"	
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"	
/lab_host="DH10B"	
/note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:	
XhoI; This cDNA library was constructed from mRNA isolated	
from etiolated hypocotyl tissue of 9-10 day old seedlings	
of the cultivar Williams 82. Complementary DNA was	
synthesized from mRNA using a primer consisting of a	
poly(dT) primer with a XhoI restriction site. EcoRI	
adapters were ligated to the blunt-ended cDNA fragments	
followed by digestion with EcoRI and XhoI. The cDNA	
fragments were directionally cloned into the EcoRI-XhoI	
restriction site of the pBluescript vector. The ligated	
cDNA fragments were transformed into DH10B host cells	
(Gibco BRL). This library was constructed by Dr. Randy	
Shoemaker."	
BASE COUNT	
199 a 127 c 127 g 136 t	
ORIGIN	
Query Match	31.7%; Score 313.2; DB 14; Length 589;
Best Local Similarity	73.3%; Pred. No. 8.3e-67;
Matches 415; Conservative	0; Mismatches 148; Indels 3; Gaps 1;
49 AGAGCCACAAGACCATTTTCTTCTGTAAACCTCTGTATATAGCCATGGCTTT	108
1 1	
27 ACACCAAAAGGATCATATATCTTGTTGACACCTTGTAAGTGAAGAAATATGSCATTT	86
109 GCAGGACCCACACAGAAATGCATGGCATGTGACAGACGTCTATCTGTGGTACAAATTA	168
1 1	
87 GCAGGAAACACTCAAGATGATGCGCTGTGACAAACAGTTTATCTGTTGATTAAGTT	146
169 ACTGAGATTAACAGAAATCTATTCACAAACCTGTTCAATCGCATCTGCAAGGCACT	228
1 1	
147 ACCGAGATTAACCGAGTATACATTAAGCTTGGCTTCAATGCCACACCTGCAAAAGAAC	206
229 GTCAAGCTTGGCAATACAAATTCCTTTAGGAGATTCATATCTGTAAGACACACATTTG	288
1 1	
207 CTCGAAGCTCAGCAACTATTAATCTTTTGAAGAGATCTTTTACTGAGGCGACACTTTG	266
289 CAGCTCTTCAACAACAACTGCGAGTTTGATTAAGCTTTGAAGGTACCAACAAAATGTG	348

[illegible]

Db 65 ATGCATCACCCTTGGAGGAAACCAACAAAATGCATGCCCTGTGACAAAACCTGTGAC 124

Qy 154 CTGGTTGACAAATTTAACTGACAGATTAACGAATCTATCAACAAAGCTTGTTCAGATGCCAT 213

Db 125 CTGTGTGATTAAGTTAGCGCCGATTAATGGGTCTATCAACAAAGCTTGTTCAGATGCCAT 184

Qy 214 CACTGCAAGGCGACGTCAAGCTTGGCACTACAAATTCCTTTGAGGAGTCTATACGT 273

Db 185 CATTGCAAGGAAACCCCTCAAGCTCAAGCTCAATTCCTTTGAGGAGTCTATACGT 244

Qy 274 AGACGACCTTTGATGACCTCTTCAACAACTGGCATTGGATTAACAAAGCTTTGAAGCT 333

Db 245 AGGCTCACTTTGATGACCTCTTCAAGAGAACTGGCAGCTTGAAGAAAGCTTTGAAGGA 304

Qy 334 ACACCAAAAATTTGAAAGCCACAGAAACCCATTTGACAGTGAAGAAACAGATGACCAA 393

Db 305 ACACCAAAAGATTTGAAAGCTTGAAGCTTGTGAAATGACAAATGACAG-----AAA 358

Qy 394 GTGACAGCATGTTTGGTGAACAAGAAATGTTTGGCTGCAAGAAACCTGTCTAC 453

Db 359 GTCTCCAAAGATTTGTGGGACACAGATTAATGTGTGGATGCGATAGGACTGTTAT 418

Qy 454 CCACAGAAAAGTATCAGCAATGGCAGCCATATCCATTAAGAGTGTCTTCAATGACAG 513

Db 419 CCAACTGAAAGGTTTCTGTAATAGCGCCGATATATCAGAGAGCTGTCAAGTGCAGC 478

Qy 514 CACGAGGCTGTGTAATAGCCCTTCCAACTATACCCGACATGAGGAGGCTTATATGT 573

Db 479 CATGAGGCTGTGACCATGAGCCATCAATATATGTCCTGAGGAGAACTCTACAGC 538

Qy 574 AAACATCCCATATTTCAACCTTATCAAGAGAAAGGCACTTAAGCAAGCTTGAAGGTGAC 633

Db 539 AAGCATCATCAATACAACTCTTCAAGGAGAAAGAACTACAGCAGCTTGAAGGTGAT 598

Qy 634 CATGAATGAAT 645

Db 599 CTGAGAGAGCT 610

RESULT 14
BF638624 657 bp mRNA linear EST 19-DEC-2000
LOCUS NF062F05PL1F1045 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION
ACCESSION BF638624
VERSION BF638624.1 GI:11902782
KEYWORDS EST.
SOURCE barbel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE 1 (bases 1 to 657)
AUTHORS Liu,D., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
TITLE 'H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
JOURNAL Expressed Sequence Tags from the Samuel Roberts Noble Foundation
COMMENT Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 657 Std Error: 0.00
Plate: 062 Row: F Column: 05
Seq primer: TCACACGAAACGATATGAC.
FEATURES
source location/Qualifiers
1..657
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/db_xref="taxon:3880"

/clone="NF062F05PL"
/clone_id="phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20um potassium
phosphate. RNA was prepared from above ground tissues."

BASE COUNT 211 a 122 c 125 g 192 t 7 others
ORIGIN

Query Match 31.4%; Score 310.2; DB 12; Length 657;
Best Local Similarity 77.7%; Pred. No. 4.7e-66;
Matches 383; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

Qy 100 ATGCTTTGAGAGAACACACAGAAATGATGATGATGATGATGATGATGATGATGATGAT 159

Db 166 ATGCAATTTGAGAGAACACACAGAAATGATGATGATGATGATGATGATGATGATGATGAT 225

Qy 160 GACAAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 219

Db 226 GATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 285

Qy 220 AAGGCACTGTCAGAGCTTGGCACTACAAATCTTTGAGGAGTCTTATACGTGAGACCA 279

Db 286 AAAGAACCCCTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 345

Qy 280 CACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 339

Db 346 CACTTCGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 405

Qy 340 AAAATGTAAGGACACAGAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 399

Db 406 AAAATGTAAGGACACAGAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 465

Qy 400 AGCATGTTTGGTGAAGAGAGAGAAATGTTTGGCTGCAAGAAACCTGTACCCACAA 459

Db 466 AGTATGTTTGGTGAAGAGAGAGAAATGTTTGGCTGCAAGAAACCTGTACCCACAA 525

Qy 460 GAAAGATATGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519

Db 526 GAGAGAT 585

Qy 520 GGCTGTGAATTAAGCCCTTCCAACTATACGCAATGATGATGATGATGATGATGATGATGATGAT 579

Db 586 NGTGTACTATCACTCTTCC-ATTACATGACCATGATGATGATGATGATGATGATGATGATGAT 644

Qy 580 CACCATATTCAC 592

Db 645 CACCATATTCAC 657

RESULT 15
BM178858 535 bp mRNA linear EST 06-DEC-2001
LOCUS sa360d07.y1 Gm-c1072 Glycine max cDNA clone SOYEAN CLONE ID:
DEFINITION Gm-c1072-4021 5' similar to TR:Q9SP54 Q9SP54 LIM DOMAIN PROTEIN
WUIML.; mRNA sequence.
ACCESSION BM178858
VERSION BM178858.1 GI:17402076
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 535)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corryell,V., Khanna
TITLE 'A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers

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